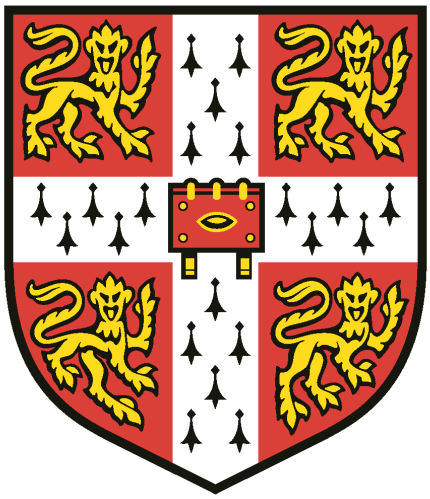
Dynamics of the Human Gut Microbiota in Very Early Life



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This dissertation is submitted for the degree of

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Declaration

This dissertation is the result of my own work and includes nothing which is the outcome of work done in collaboration except specified in the text. It is not substantially the same as any that I have submitted, or, is being concurrently submitted for a degree or diploma or other qualification at the University of Cambridge or any other University or similar institution. No substantial part of my dissertation has already been submitted, or, is being concurrently submitted for any such degree, diploma or other qualification at the University of Cambridge or any other University or similar institution. This thesis does not exceed the length limit of 60,000 words specified by the Biology Degree Committee.

Yan Shao

September 2019

Summary

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Immediately after birth, newborn babies experience rapid colonisation by microorganisms from their mothers and the surrounding environment. Diseases in childhood and later in life are potentially mediated through perturbation of the infant gut microbiota colonisations. However, the impact of modern clinical practices, such as caesarean-section delivery and antibiotic usage, on the earliest stages of gut microbiota acquisition and development during the neonatal period (≤1 month) remains controversial. In this thesis, I generated and analysed the largest datasets of shotgun metagenomes, isolate genomes and metagenome-assembled genomes of the neonatal gut microbiota to date.

In the largest birth cohort study of its kind, I profiled the gut microbiomes of 771 UK healthy term infants and mothers through shotgun metagenomic sequencing 1,679 longitudinal faecal samples. Here I report that the mode of delivery is a significant factor that affects the composition of the gut microbiota throughout the neonatal period, and into infancy. This is evident by the disrupted transmission of maternal *Bacteroides* strains, and high-level colonisation by opportunistic pathogens associated with the hospital healthcare environments (including *Enterococcus*, *Enterobacter* and *Klebsiella* species), in babies delivered by caesarean section. Furthermore, I validated culture-independent detection of pathogen species by matched large-scale culturing, and whole-genome sequencing of over 800 bacterial strains cultured from these babies identified virulence factors and clinically relevant antimicrobial resistance in opportunistic pathogens that may predispose to opportunistic infections. These findings highlight the critical role of the local environment in establishing the gut microbiota in very early life, and identify colonisation with antimicrobial-resistance-containing opportunistic pathogens as a previously underappreciated risk factor in hospital births.

Acknowledgements

First and foremost, I would like to thank my supervisor Trevor Lawley and external supervisor Nigel Field, for giving me the opportunity to work on this exciting project, and the freedom to explore my own ideas. Trevor, I am very grateful for your continuous guidance, trust and support throughout the ups and downs of my PhD journey.

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Lastly, I would like to thank my family and friends, near and far, for their love and support. I am forever grateful to my parents and grandparents for their unconditional support in everything I do from 10,000 km away. Thanks to Edward, Yan Zi, Hanwei, Betty, Luis, Ben, Hark, Sophie, Chen and Jingyi for all the fun times, and your encouragement in the stressful times. I wouldn't have made it through without you.

Publications

Shao, Y., Forster, S. C., Tsaliki, E., Vervier, K., Strang, A., Simpson, N., Kumar, N., Stares, M. D., Roger, A., Brocklehurst, P., Field, N., Lawley, T. D. (2019) Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. *Nature*. 574 (7776), 117-121.

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Contributions

This thesis is the result of my own work except:

- The Baby Biome Study sampling strategy was developed by Sam Forster, Trevor Lawley, Nigel Field (UCL), Alison Rodger (UCL) and Peter Brocklehurst (UCL/Birmingham) prior to the start of this thesis;
- The faecal sample collection and processing protocols were developed by Sam Forster, Evdokia Tsaliki (UCL), Nitin Kumar and Mark Stares through pilot experiments prior to the start of this thesis;
- Participant recruitment and raw clinical metadata collection were carried out by the Baby Biome Study research midwives;
- Raw faecal sample storage, processing and metagenomic DNA extraction were performed by the Baby Biome Study research technicians N. Moreno, H. Ali, S. Bibi and A. Takyi;
- DNA sequencing and data storage were performed by the Core Sequencing pipeline and Pathogen Informatics teams at Wellcome Sanger Institute, respectively;
- Bacterial DNA extraction was performed with assistance from Mark Stares;
- Count of the maternal strain transmission events was computed by Kevin Vervier, who also generated the plot to visualise individual species transmission events (Figure 2.13b);
- The plots showing the gut microbiota stability (Figure 2.2c-d) were generated by Kevin Vervier;
- Meta-analysis of the opportunistic pathogen carriage in previous studies (Section 3.3.5) was conducted with assistance from Kevin Vervier.

Abbreviations

16S	16s rRNA gene sequencing
AMR	Antimicrobial resistance
ANI	Average Nucleotide Identity
BBS	Baby Biome Study
BLAST	Basic Local Alignment Search Tool
C-section	Caesarean section
CGR	Culturable Genome Reference
DNA	Deoxyribonucleic acid
EBI	European Bioinformatics Institute
GTDB	Genome Taxonomy Database
GVD	Gut Virome Database
HGG	Human Gastrointestinal Bacteria Genome
HMO	Human milk oligosaccharides
HMP	Human Microbiome Project
HQ	High-quality
IAP	Intrapartum antibiotic prophylaxis
MAG	Metagenome-assembled genome
NCBI	National Center for Biotechnology Information
NHS	National Health Service
NICE	National Institute for Health and Care Excellence
NMDS	Nonmetric multidimensional scaling
OTU	Operational taxonomic unit
PCR	Polymerase chain reaction
PERMANOVA	Permutational multivariate analysis of variance

qPCR	Quantitative PCR
RefSeq	NCBI reference sequence database
SNP	Single-nucleotide polymorphism
TEDDY	The Environmental Determinants of Diabetes in the Young
UK	United Kingdom
UMGS	Unclassified metagenomic species
WGS	Whole-genome sequencing
WHO	World Health Organization

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Chapter 1: Introduction

1.1 The human gut microbiota

The human gastrointestinal tract is colonised by a dense and diverse community of resident commensal microorganisms known as the gut microbiota. These microorganisms include numerous and diverse bacteria, fungi, viruses, archaea, and protozoa. The bacterial portion of this population makes up the larger proportion in terms of mass (Qin *et al*., 2010; Yatsunenko *et al.*, 2012), and has the largest influence of the intestinal microbiota on human health. It is believed to add approximately 38 trillion cells to the body of a healthy adult, a number that is in the same order of magnitude with the number of cells in an adult human body (Sender *et al.*, 2016).

The human gut microbiota has coevolved with the human host to perform functions that the host cells are lacking – providing nutrient breakdown from food (Sonnenburg, Bäckhed, 2016), calibrating the immune system (Hooper *et al.*, 2012), modulating host response to immune-mediated therapies (Gopalakrishnan *et al.,* 2018; Routy et al., 2018) and defending against pathogens (Bäumler, Sperandio, 2016). Indeed, the human gut microbiome, representing the genetic repertoire encoded by the human gut microbiota, is estimated to be at least two orders of magnitude larger than the number of genes in the human genome (Qin *et al.*, 2010). Based on the mutualism between the host and its microbiome, it has been suggested that we are all holobionts, entities which consist of ourselves and our microbiomes (Bordenstein, Theis, 2015). Intriguingly, recent studies have demonstrated a causal role of gut microbiome-encoded genes and metabolites in the development of metabolic diseases (Koh *et al.*, 2018; Hoyles *et al*., 2018; Duan *et al.*, 2019). However, the dynamics of the gut microbial ecosystems, as well as the complexity of their functions and host-microbiome interactions, remain largely unexplored.

Historically, studies on the human gut microbiota were based on microbial culturing, which is limited by the "culturability" of only a fraction of the entire microbial community (Steen *et al.*, 2019), and does not permit full assessment of the entire community. According to the most recent estimate, over 70% of the human gut microbiota species remain uncultivated (Almeida *et al.*, 2019a). This limitation is circumvented through the recent developments and applications of 16S rRNA gene sequencing and shotgun metagenomic sequencing, the latter of which has enabled comprehensive taxonomical and functional characterisation of the whole human gut microbial community in an unbiased manner and at a population scale across the globe (Qin *et al.*, 2010; Falony *et al.*, 2016; Zhernakova *et al.*, 2016). Whilst these sequencing-based, computational studies have tremendously increased our knowledge about the diversity of the microbiome and its implications in health and diseases, hypotheses generated *in silico* require experimental validations using gut bacterial strains that can be challenging to isolate and cultivate in the laboratory. This technical constraint has been largely overcome through recent advances in high-throughput anaerobic culturing techniques using a wide variety of culture media and growth conditions, which have enabled the isolation of the majority of the diverse human gut microbiota (Goodman *et al.*, 2011; Lagier *et al.*, 2016; Browne *et al.*, 2016), in addition to the creation of multiple collections of cohort-specific gut bacteria in pure cultures and genomes, many of which are novel (Forster *et al.*, 2019; Zou *et al.*, 2019; Poyet *et al.*, 2019). These continually expanding resources greatly complement the genomic analysis of the human gut microbiota with improved taxonomic resolution and enable experimental validation of disease causation (Neville *et al.*, 2018). Together with other 'omics' technologies, including RNA sequencing, single-cell sequencing, metabolomics and proteomics (Zhou *et al.*, 2019; Lloyd-Price *et al.*, 2019), metagenomics and culturing are revolutionising the field of human gut microbiota research (Figure 1.1), and enabling the potential to elucidate complex dynamics of the human gut microbiota and allow unprecedented hypothesis-driven research.

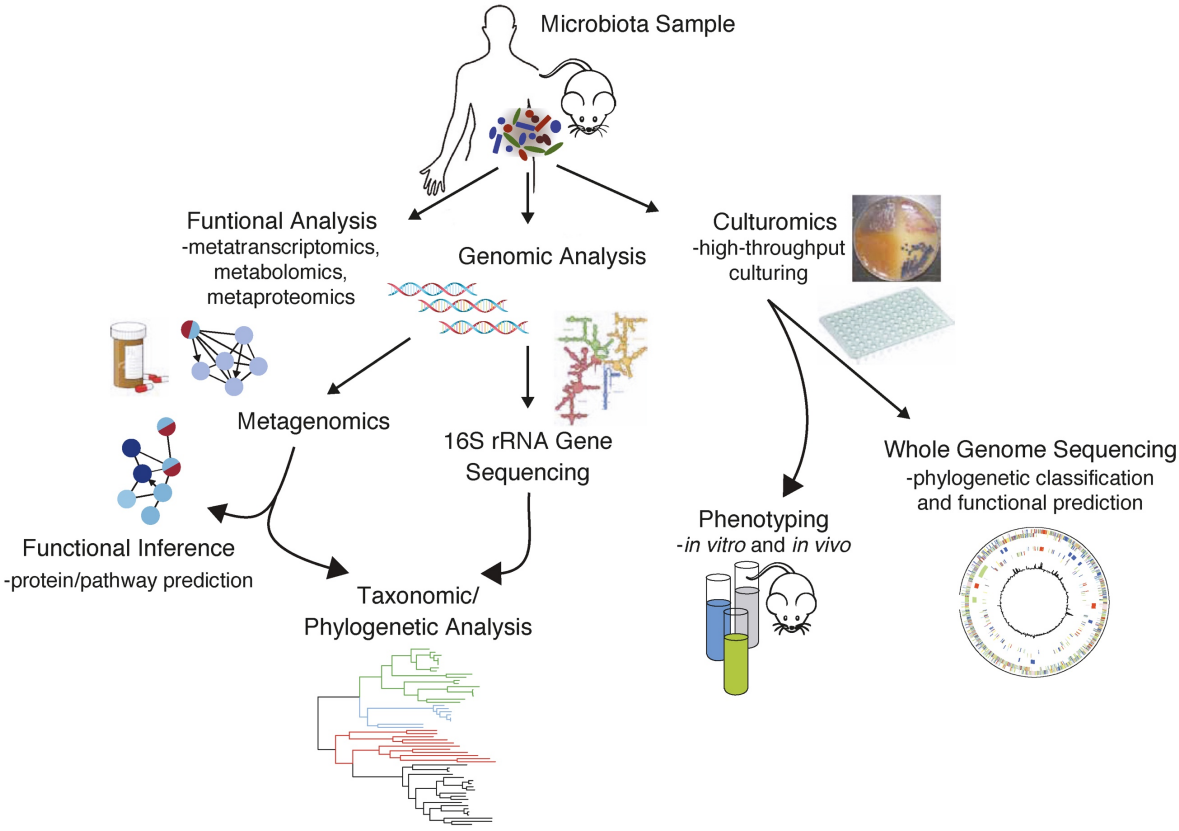

Figure 1.1 High-throughput sequencing and culturing methods applied in microbiota research.

The taxonomic and functional capacity of the gut microbiota can be assessed using various high-throughput 'omics technologies, primarily with amplicon sequencing of the 16S rRNA genes and shotgun metagenomics (direct sequencing of the total DNA), and additionally using RNA-sequencing or metatranscriptomics to detect temporal functional activity), and metabolomics to detect metabolites. An increasing proportion of gut bacteria can now be isolated and cultured by high-throughput techniques. The resulting microbes can then be whole-genome sequenced to examine their genetic traits, or experimentally studied with *in vitro* or *in vivo* assays. A combination of these complementary approaches is rapidly expanding our understanding of the microbiota during health and disease. Sourced from Pham, Lawley, 2014.

1.2 Early-life human gut microbiota and implications for health and disease

Whist the majority of earlier landmark studies have focused on the gut microbiota of mature adults, the establishment and development of the gut microbiota in early life had received an increasing amount of interests in recent years, owing to its important implications in metabolic and immunological programming in early life (Prescott, 2013), and potentially in later life health outcomes (Tamburini *et al.*, 2016).

The first years of our lives represent a critical period of environmental exposures. The microbial exposure of immune cells during this early period is considered a "window of opportunity" for the proper immune education, and establishment of immune tolerance to the developing commensal microbiota (Gensollen *et al.*, 2016). The view that immune regulation is driven by host-microbiota interactions was first outlined by Dr David Strachan in 1989 as the "hygiene hypothesis". He proposed that reduced microbial exposure in early life, through improved hygiene conditions and low incidence of infection in early childhood, is linked to the rise in allergic disease in 20th-century urban societies (Strachan, 1989).

Several *in vitro* and *in vivo* studies have since demonstrated regulation of early-life immune system by microbiota community and individual microbiota members, the latter of which were further associated with later-life development of atopy and asthma in human patients (Arrieta *et al.*, 2015; Fujimura *et al.*, 2016; Stokholm *et al.*, 2018). In mice, the exposure to maternal microbiota metabolites *in utero* and postnatally via breast milk feeding was shown to prime the neonatal innate immunity with increased group 3 innate lymphoid cells (Gomez de Agüero *et al.,* 2016). In mouse studies, commensal colonisation of the neonatal gut microbiota was shown to play a prominent role in the regulation of invariant natural killer T cells (Olszak *et al.*, 2012; An *et al.,* 2014), T cell differentiation (Fujimura *et al.*, 2016) and IgE antibodies (Cahenzli *et al.,* 2013), the lack of which would increase late-life susceptibility to inflammatory diseases. Regarding the prevalent pioneering colonisers of the neonatal gut microbiota, the exposure of

Bacteroides-derived lipopolysaccharides was shown to trigger immune suppression in the onset of autoimmunity *in vivo* (Vatanen *et al.,* 2016; d'Hennezel, *et al.*, 2017); while *Bifidobacterium* spp. were known to exert strain-specific immunomodulatory effects directly through their surface-associated molecules or indirectly via metabolism and cross-feeding of the otherwise non-digestible host-derived glycans such as human milk oligosaccharides (HMOs) in breast milk (Fanning *et al.,* 2012; O'Neill *et al*., 2017).

Furthermore, disruption of host-microbiota metabolic interaction during this critical early window was also shown to affect infant growth via degradation of non-digestible oligosaccharides in breast milk (Blanton *et al.*, 2016; Baumann-Dudenhoeffer *et al.*, 2018), and the long-term predisposition to diet and antibiotics-induced metabolic diseases as observed in mice (Cox *et al.*, 2014; Livanos *et al.*, 2016).

From an ecological point of view, the initial colonisation process of the human gut microbiota represents the *de novo* assembly of a microbial community (Costello *et al.*, 2012), which is influenced by both environmental (e.g., mode of delivery, mode of feeding, antibiotic usage) and host factors (Planer *et al.*, 2016; Pabst *et al.*, 2016). Whilst these aspects have been comprehensively discussed in several recent reviews (Milani *et al.*, 2017; Korpela, de Vos, 2018; Robertson *et al.*, 2019; Derrien *et al.*, 2019), in this chapter I will focus on summarising the current knowledge of the "normal" colonisation trajectory in early life, and the most important perturbation factors including caesarean-section delivery and antibiotics (Figure 1.2).

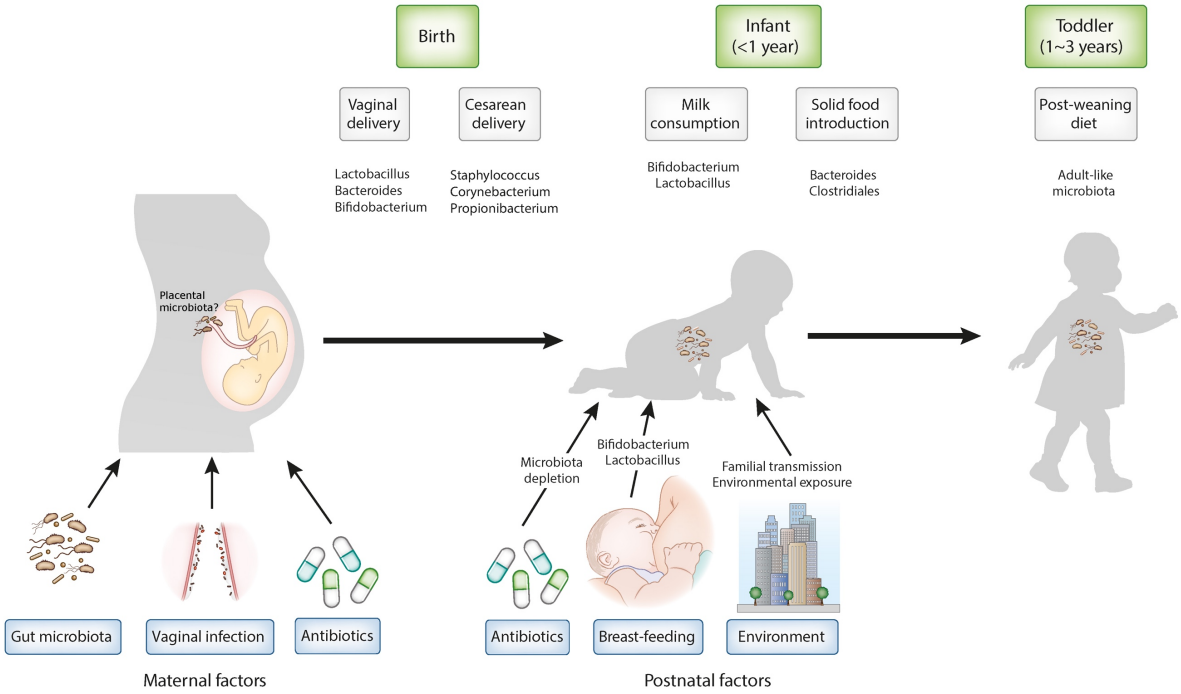

Figure 1.2 Perinatal factors shaping the early-life gut microbiota.

Maternal and postnatal factors that can influence the development of the gut microbiota in the perinatal period and throughout infancy, until it matures towards an adult-like state by age 3. Bacteria associated with the different processes based on literature are indicated. Adapted from Tamburini *et al.*, 2016.

1.3 Developmental trajectory of early-life gut microbiota

Characterisation of the gut microbiota community represents the first step in understanding the development of early-life gut microbiota. Historically, identification of gut bacteria from infant faeces was based on culturing, usually with selective media for screening bacteria of interests (Brook *et al.*, 1979; Bennet *et al.,* 2002; Hascoët *et al.,* 2011). Prior knowledge of the target bacteria is needed to enable successful cultivation, insights derived from culture-dependent studies were thus limited to a minimal number of then 'culturable' aerobic bacteria (e.g. *Enterobacteriaceae*, *Enterococcus, Streptococcus*), and did not permit the quantitative measurements of bacteria within the community.

Due to these limitations, culture-independent approaches have been utilised to gain more detailed insights into the common bacterial colonisers across different stages in the first years of life (Adlerberth and Wold, 2009). These 'first-generation' molecular techniques, including denaturing gradient gel electrophoresis (Favier *et al.*, 2002), real-time polymerase chain reaction (Hopkins *et al.*, 2005; Penders *et al.*, 2005, 2006), dot-blot hybridization, phylogenetic microarrays (Palmer *et al.*, 2007), and fluorescent *in situ* hybridization with flow cytometry (Harmsen *et al.*, 2000; Kirjavainen *et al.*, 2002; Fallani *et al.*, 2010), have mainly targeted the 16S rRNA gene present in all prokaryotes. In comparison to cultivation studies, these molecular techniques are rapid, and enable quantification of bacteria, thus providing a less biased snapshot of the infant gut microbiota (Adlerberth and Wold, 2009). However, they are still relatively laborious, poor taxonomic resolution and prone to PCR bias, thus precluding phylogenetic and proportional inference, and comparison of microbiota compositional profiles between samples and studies.

It was not until the advent of high-throughput DNA sequencing that has since greatly facilitated the phylogenetic and longitudinal characterisation of the infant gut microbiome profiles in a comprehensive and robust fashion. Indeed, most of our current knowledge of infant gut

microbiota development is derived from a bloom of microbiome sequencing studies over the past decade. Importantly, most earlier observations based on culture-dependent and sequencing-independent approaches have been validated by sequencing studies. For this reason, the rest of this chapter will primarily focus on discussing the findings from sequencing-based studies, unless otherwise stated.

The early-life gut microbiota colonisation is assumed to begin during and after birth, as the neonatal gut microbiota is exposed, and rapidly colonised by a wide variety of microbes from the mothers and surrounding environment (Dominguez-Bello *et al.*, 2010). This traditional view, operating under the dogma of a sterile *in utero* environment, has been challenged by a claim of the existence of "placental microbiota" (Aagaard *et al.*, 2014). However, the evidence for this was limited to the detecting of DNA in very low biomass sample, rather than viable bacterial cells. Recently, several recent studies provided concrete evidences to suggest that microbial DNA detected in placental samples were contaminant in sample processing, concluding that no placental microbiome exists in healthy pregnancy (Perez-Muñoz *et al.*, 2017; Leiby *et al.*, 2018; Theis *et al.*, 2019; de Goffau *et al.*, 2019).

Immediately after birth, the gut microbiota undergoes fast environmental transitions from being oxygen-rich to facultative anaerobic, and then strict anaerobic over a period of days (Avershina *et al.*, 2014; Jost *et al.*, 2012; Pantoja-Feliciano *et al.*, 2013). Although there has been no direct experimental evidence, the neonatal gut microbiota is thought to be an aerobic environment, which coincides with the early appearance of facultative anaerobic bacteria, such as *Enterobacteriaceae, enterococci, streptococci* and *staphylococci* (Palmer *et al.*, 2007; Bäckhed *et al.*, 2015). It has been hypothesised that the relatively high level of oxygen in the neonatal gut during the first few days of life could favour the colonisation of these facultative bacteria, which consume oxygen and lower the redox-potential in the gut (Penders *et al.*, 2006).

The resulting anaerobic environment, in turn, enables the subsequent colonisation of obligate anaerobes such as *Bacteroides* and *Bifidobacterium* species (Bäckhed *et al.*, 2015; Bokulich *et*

al., 2016), which proliferate as they are capable of utilising human milk oligosaccharides as well as similar structures in the host-produced mucus. The dominance of HMO-utilising bacteria prevail for the majority of the infancy, which is predominantly driven by the breastfeeding status (Koenig *et al.*, 2011; Bäckhed *et al.*, 2015; Bokulich *et al.*, 2016; Stewart *et al.*, 2018), with non-breastfed (i.e. formula-fed) infants depleted in the level of *Bifidobacterium* (Yatsunenko *et al.*, 2012; Bäckhed *et al.*, 2015; Bokulich *et al.*, 2016; Stewart *et al.*, 2018; Vatanen *et al.*, 2018). Interestingly, the composition of HMOs is influenced by host genetic factors, such as the *FUT2* genotype for secretor status (Korpela *et al.*, 2018a), whilst the most dominant sub-species of *Bifidobacterium* (*B. longum, B. breve, B. bifidum*) were shown to be specialised in utilising different HMOs in mother's breast milk (Vatanen *et al.*, 2019). These results highlight a form of maternal genetic "imprint" on the infant gut microbiota via selective colonisation of *Bifidobacterium* strains through breastfeeding. The cessation of breast milk feeding (usually by 12 month of age), rather than the introduction of more varied, solid foods, signals a major shift in the gut microbiota composition as bifidobacteria are replaced by a diverse group of fibre-degrading Firmicutes (Bäckhed *et al.*, 2015; Stewart *et al.*, 2018). Whilst breastfeeding is known to favour the colonisation of probiotic and breast milk-associated *Bifidobacterium* and *Lactobacillus* strains, exclusive infant feeding of formula (i.e. without HMOs) in infancy is associated with higher microbial diversity and levels of adult-like taxa including *Bacteroides* and *Clostridium,* which have been consistently reported in studies based on different molecular technologies (Penders *et al.*, 2005; Bezirtzoglou *et al.*, 2011; Backhed *et al.*, 2015). Nevertheless, it remains to be determined the exact role of the more heterogenous formula diet, independent of the lack of breast milk feeding.

Furthermore, the increase in observed bacterial diversity contributes to changes in microbiota functions, most notably an overall increase in short-chain fatty acids (SCFAs) such as butyrate (Koenig *et al.*, 2011), and induction of genes responsible for the degradation of complex carbohydrates and starch (Koenig *et al.*, 2011). By 2-3 years of age, the gut microbiota matures

to closely resemble the adult composition (Koenig *et al.*, 2011; Yatsunenko *et al.*, 2012; Bäckhed et al., 2015; Stewart *et al.*, 2018), which is functionally more complex and adapted to metabolise proteins, resistant starch and plant-derived complex carbohydrates in the adult diet (Bergström *et al.*, 2014). Collectively, these findings indicate that early-life gut microbiota development and maturation in the first three years of life are primarily driven by changes in diet, as evident by the strong selection effect favouring the gut microbes functionally adapted to the changes in substrate availability (Figure 1.2).

1.4 Perturbations of the early-life gut microbiota

1.4.1 Caesarean-section delivery

The most common perturbations to the gut microbiota development are caesarean-section delivery and perinatal antibiotics, the latter of which is also involved in caesarean-section delivery. In the UK, mothers are administered with prophylactic intravenous broad-spectrum antibiotics 60 minutes prior to skin incision in the caesarean section to reduce maternal postpartum infection (NICE, 2011).

Caesarean section - the most common surgery in many countries around the world (Wells *et al.*, 2019) - is a life-saving intervention for women and babies when complications occur during pregnancy or birth. The global use of caesarean section had almost doubled in the past 15 years from 12.1% in 2000 to 21.1% in 2015, with the highest rates recorded in Latin America (Wells *et al.*, 2019, Figure 1.3).

In the UK, caesarean-section deliveries have increased from 19.7% of births in 2000 to 28.4% in 2019 (NHS, 2019), well in excess of the 10–15% of births considered optimal by the recommendation of the World Health Organisation (WHO, 2018). This rise is largely driven by increases in non-medically indicated caesarean section that does not offer significant maternal or perinatal benefits, but is instead associated with considerable risks of maternal mortality and morbidity, and neonatal risks including increased likelihood of allergy, atopy, and asthma

(Sevelsted *et al.*, 2015; 2016; Thavagnanam *et al.*, 2008; Sandall *et al.*, 2018). Very recently, both the WHO and the International Federation of Gynaecology and Obstetrics issued evidence-based guidance calling on public health stakeholders to reduce unnecessary caesarean sections (WHO, 2018; Visser *et al.*, 2018).

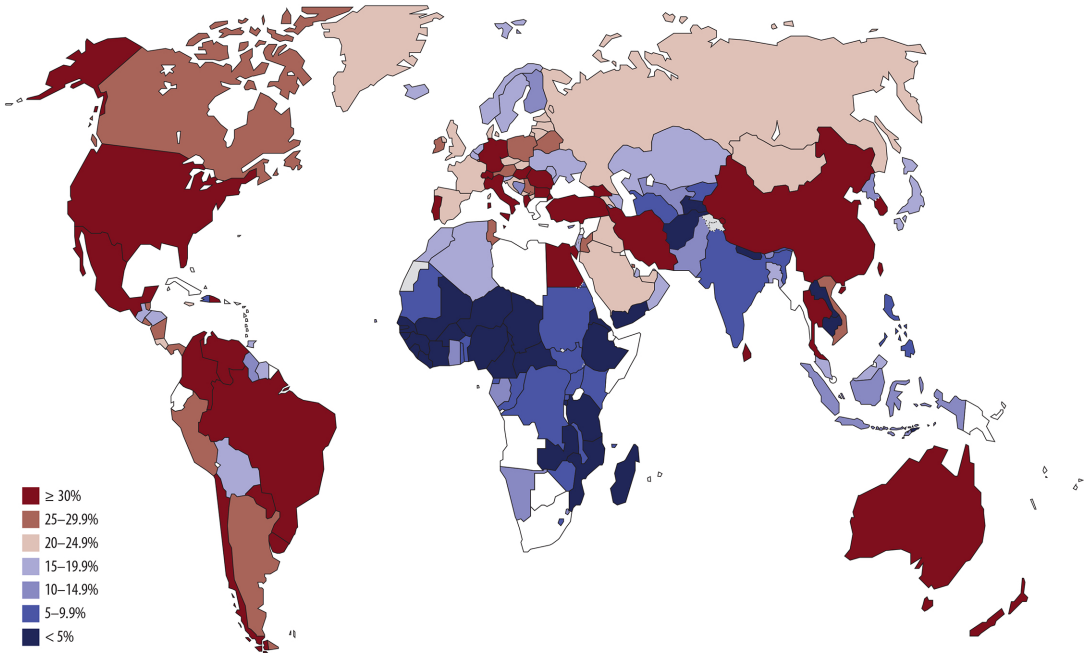

Figure 1.3 Current rates of caesarean section worldwide

Caesarean section rates in 150 countries according to the nationally-representative data collected as of 2014. Sourced from Betrán *et al.,* 2016.

Bacteria encountered by the neonate with vaginal birth have been reported to be very different than those experienced with caesarean-section birth (Dominguez-Bello *et al.*, 2010). The initial "maternal seeding" of the newborn to microbes happens during the delivery process and is strongly affected by the delivery mode. In vaginal birth, the initial microbiota of newborns is determined by the maternal vaginal microbiota as he or she passes through the birth canal, which is predominated by *Lactobacillus* (Dominguez-Bello *et al.*, 2010; 2016). However, a more important role of vaginal delivery might be promoting faecal-oral transmission of maternal gut microbiota (Lozupone *et al.*, 2012), which would explain the source of highly enriched, faecal-associated bacteria in vaginal delivery newborns (Makino *et al.*, 2013; Bäckhed et al., 2015; Yassour *et al.*, 2016; Bokulich *et al.*, 2016; Rudi *et al.*, 2012). Indeed,

recent metagenomics studies have identified vaginal birth-associated, strain-specific links of *Bacteroides* and *Bifidobacterium* between paired neonatal and maternal gut microbiota samples, indicative of a prominent route for the maternal gut microbiota transmission through vaginal birth (Bäckhed et al., 2015; Yassour *et al.*, 2018; Ferretti *et al.*, 2018; Korpela *et al.*, 2018b; Wampach *et al.*, 2018).

By comparison, this route is thought to be broken during caesarean-section delivery. Consequently, caesarean-section infants are more exposed to colonisation by skin bacteria such as *Staphylococcus*, *Corynebacterium*, and *Propionibacterium* (Dominguez-Bello *et al.*, 2010) potentially from the mother's skin and/or staff in the operating room (Shin *et al.*, 2015). In addition, caesarean sections newborns were also found to carry bacteria carried by hospital staff and in the operating room (Shin *et al.*, 2015) and neonatal intensive care unit (Brooks *et al.*, 2014), such as *Clostridiales[Clostridium] difficile* (Penders *et al.*, 2005; 2006). So far, the most common microbial signature of caesarean-section-delivered infants is the disturbed microbiota maturation trajectory and delayed colonisation of *Bacteroides*, which persist well beyond 1 year (Salminen *et al.*, 2004; Jakobsson *et al.*, 2014; Bäckhed et al., 2015; Yassour *et al.*, 2016; Bokulich *et al.*, 2016). In addition to its direct impact on microbial exposure, caesarean section involves antibiotic prophylaxis, which could affect bacterial colonisation from pre-labour rupture of membranes. Furthermore, caesarean section can cause delayed onset of breastfeeding (McDonald *et al.*, 2012), which can result from the lack of immediate skin contact (that facilitates breastfeeding), and/or insufficient lactation through disrupted hormone-stimulated lactogenesis due to stress associated with complications during abdominal surgery (Hobbs *et al.*, 2016).

Whilst it has become clear that the mode of delivery is a significant factor in shaping the gut microbiota during the first 2-3 years of life, its role in the highly dynamic turnover during very early life have not been thoroughly examined. Prior to three months of age, the observed effect of caesarean section on the gut microbiota composition is stronger than breastfeeding (Madan

et al., 2016), and without interactive effect with breastfeeding status (Azad *et al.*, 2016). Interestingly, a recent high-profile study reported highly contradictory results of ubiquitous detection of *Bacteroides* in caesarean-section infants (n = 12), and no difference (P = 0.057) in the microbiota composition between 6-week-old infants born via caesarean section and vaginal delivery (Chu *et al.*, 2017). Interestingly, this finding could not be repeated upon re-analysis (Korpela, de Vos, 2018).

1.4.2 Antibiotics exposure

It is estimated that up to 40% of newborn babies are indirectly exposed to maternal intrapartum antibiotic prophylaxis (IAP) administered during vaginal delivery (Stokholm *et al.*, 2013). IAP, which involves intravenous penicillin, or vancomycin/cefuroxime in case of penicillin allergy in labour in the UK (Hughes *et al.,* 2017), constitutes a standard of care to prevent neonatal Group B *Streptococcus* (GBS) sepsis and maternal infection after caesarean section (van Schalkwyk *et al.*, 2010). After birth, babies are frequently subjected to direct administration of antibiotics, which represent the majority of prescription medication used by children in the United States (Chai *et al.*, 2012).

Usage of IAP for GBS has been linked to amoxicillin resistant late-onset *E. coli* infections in hospitalised infants (Didier *et al.*, 2011). Since all caesarean-section deliveries receive IAP, the microbiota perturbation effects observed with IAP exposure in vaginal birth should allow assessment of the independent effect of antibiotics, separately from caesarean sections. In term infants, the perturbation effect of IAP in vaginal birth appeared to be weaker than caesarean section in previous studies, which also reported decreased alpha diversity (Mazzola *et al.*, 2016; Nogacka *et al.*, 2017), the reduced abundance of commensal *Bacteroides*, *Parabacteroides* and *Bifidobacterium* in 1-week old neonates (Mazzola *et al.*, 2016; Nogacka *et al.*, 2017), in 3-month-old term infants after maternal IAP (Azad *et al.*, 2016; Arboleya *et al.*, 2015), which also had increased level of the family *Clostridiaceae* (Azad *et al.*, 2016) and environmental-associated *Klebsiella* and *Staphylococcus* species at one-month-old (Stokholm *et al.*, 2016).

Interestingly, exclusive, but not partial breastfeeding during the first three months of life seemed to alleviate the effect of IAP (Azad *et al.*, 2016), indicating potential microbiota-mediated protective effects of breastfeeding against the damage of IAP.

The effect of postnatal antibiotic exposure on decreasing gut microbiota richness and diversity has primarily been observed in preterm neonates (Gibson *et al.*, 2015; Rose *et al.*, 2017; Greenwood *et al.*, 2014; Arboleya *et al.*, 2015; Gasparrini *et al.*, 2016), and also in full-term babies who received multiple antibiotic courses during infancy (Yassour *et al.*, 2016; Bokulich *et al.*, 2016; Korpela *et al.*, 2016a), which were shown to result in a pro-inflammatory state and delayed microbiota development in comparison to unexposed counterparts. Antibiotic exposure in the first year of life has been associated with diabetes (Korpela *et al.*, 2017), and increased asthma risk (McKeever *et al.*, 2012), which were reported to be mediated by microbiota perturbations (Penders *et al.*, 2011; Azad *et al.*, 2014; Korpela *et al.*, 2016a), as well as a predisposition to antibiotic-associated weight gain (Penders *et al.*, 2007; Vael *et al.*, 2011; Cox *et al.*, 2014; Korpela *et al.*, 2016a). Whilst breastfeeding could protect babies against infections and overweight in later life (Hörnell *et al.*, 2013), the protective effects were weakened or completely eliminated by early-life antibiotic exposure (Korpela *et al.*, 2016b).

Repeated antibiotic exposure during infancy can lead to short-term reduced diversity and richness of the bacterial communities, with reported decreases in *Bifidobacterium* and increases in *Proteobacteria* (*E. coli*), in comparison to non-antibiotic-treated, breastfed babies. Following antibiotic treatment, the level of antimicrobial resistance genes and their host species usually returned to baseline within a few weeks (Yassour *et al.*, 2016) or up to a year (Persaud *et al.*, 2015; Korpela *et al.*, 2016b), in comparison to approximately 2 weeks observed in adult gut microbiota (Dethlefsen, Relman, 2011; Palleja *et al.*, 2018). However, such resilience to antibiotic-induced microbiota perturbations seems to depend on the type of antibiotics, and are not applicable to resistance genes on mobile genetic elements (Yassour *et al.*, 2016) that are generally not trackable using short sequencing reads.

In conclusion, the current consensus on what is considered a "normal" developmental trajectory of the gut microbiota in early life is predominantly derived from the observations in healthy, full-term birth babies who are born via vaginal delivery, exclusively or predominately breastfed and without antibiotic exposure. That being said, it remains unclear whether the minor group of exclusively formula-fed babies, who have been underrepresented in existing cohorts limited by sample size, also follow the same microbiota developmental trajectory.

The microbiota development from the first month to the first year of life (referred to hereafter as infancy period) is predominantly driven by a breast milk-based diet with strain-specific *Bifidobacterium* dominance, whereas delivery by caesarean section and antibiotic use consistently disrupt this process. However, the developmental dynamics in the first month of life (referred to hereafter as neonatal period) is not well understood, as few studies had sampled this critical period. Despite the progresses made by culture-independent approaches, along with robust epidemiological evidence linking these early-life perturbation factors with later risk of immune-mediated diseases, and mechanistic proof of microbiota's ability to recapitulate immune-modulated disease phenotypes derived from animal models, the direct causal link between early-life microbiota perturbation (to composition or specific taxa) and later disease risk has not yet been established.

1.5 Baby Biome Study

Over the last ten years, advances in next-generation sequencing have significantly advanced our knowledge of the human gut microbiota in early life. Several high-profile studies were published just over the period of this study, and provided significant insights into the developmental trajectory of the infant gut microbiota and the dominant role of breastfeeding in the first 3 years of life (Bäckhed et al., 2015; Bokulich *et al.*, 2016; Stewart *et al.*, 2018; Vatanen *et al.*, 2018). However, the dynamic microbiota colonisation events in very early life remain poorly understood, due to lack of sampling in this critical window of microbiota development

and immune modulation. In addition to the issue of under-powering due to small sample size, the majority of the studies in this area were based on 16S rRNA gene sequencing, which is limited by taxonomic resolution (Table 1.1).

In this study, the host lab (Host-Microbiota Interactions Laboratory) is leading the gut microbiome sequencing and analysis of the Baby Biome Study (BBS), which is a large UK birth cohort that primarily aims to study the gut microbiota colonisation in very early life, and how it interacts with the immune system to influence life-long health and disease (Field *et al.*, 2013). Since the beginning of the pilot phase from early 2014, over 3,500 full-term birth (37-42 gestation weeks) subjects (mother-baby pairs) have been recruited at three large hospital trusts in London and Leicester (Bailey *et al.*, 2017). Faecal samples are collected from the participating mothers at birth, and longitudinally from their babies on day 4, 7 and 21 during the neonatal period. Participants are also contacted for a follow-up collection later in infancy period between 4 and 12 months of their lives. The BBS participants are to be followed for health outcome later in life through electronic health record linkage, and the first clinical outcome (e.g. asthma, atopy) with matched faecal sampled collection will begin at age 5.

In the first half of this study (July 2016 - December 2017), I was responsible for the management of microbiota (faecal) samples and clinical metadata received by the Host-Microbiota Interaction Laboratories from participating hospitals, and the generation of metagenomic sequencing data. Overall, a total of 1,679 gut microbiotas from 771 BBS participants were sampled and whole-genome-sequenced using shotgun metagenomics. Compared with previous studies early-life microbiota studies (Table 1.1), the novelty of the BBS microbiome sampling lies in the following aspects:

- In the UK, it is the largest birth cohort, the largest metagenome-based microbiome study, and the second-largest microbiome study after the TwinsUK cohort (Goodrich *et al.*, 2016);

- In the early-life gut microbiota field, it is the second-largest single-country study after $COPSAC_{2010}$ (Stokholm *et al.*, 2018), second largest metagenome-based study after the multi-country TEDDY study (Stewart *et al.*, 2018; Vatanen *et al.*, 2018);
- In the context of the neonatal period sampling (n = 1,202), it is the first study with longitudinal sampling, and more than six times larger by the number of subjects and 12 times larger by number of samples, in comparison to the previous largest study (Bäckhed *et al.*, 2015);
- In the context of studying the effect of caesarean-section delivery, it has the highest and well-balanced proportion of samples from babies delivered by caesarean section;
- In the context of the maternal gut microbiota sampling for studying maternal transmission (n = 178), it is approximately two times larger than the previous largest study (Bäckhed *et al.*, 2015).

Study	Method	Subject (CS)	Age	Location
Baby Biome Study *Shao et al.*, 2019	Metagenomics	596 (282)	Day 4-21 Month 4-12 Mother	United Kingdom
Dominguez-Bello *et al.*, 2010	16S	11 (6)	<24 hours	Venezuela
Azad *et al.*, 2013	16S	24 (6)	Month 4	Canada
Arrieta *et al.*, 2015	16S	74 (21)	Month 3-12	Canada
Bäckhed *et al.*, 2015	Metagenomics	98 (15)	Day 4 Month 4-12 Mother	Sweden
Yassour *et al.*, 2016	16S Metagenomics	39 (4)	Month 2-36	Finland Estonia Russia
Bokulich *et al.*, 2016	16S	43 (19)	< 24 hours Month 1-36	United States
Chu *et al.*, 2017	16S Metagenomics	60 (22)	<24 hours Week 6	United States
Wampach *et al.*, 2018	16S Metagenomics	33 (13)	< 24 hours Day 3-5 Mother	Luxembourg
Stokholm *et al.*, 2018	16S	690 (152)	Week 1 Month 1-12	Denmark
Stewart et al., 2018 Vatanen et al., 2018	16S Metagenomics	810 (196)	Month 3-40	United States Finland Germany Sweden

Table 1.1 Key features of recent sequencing-based cohort studies on the early-life gut microbiota

This list summarises the methods, sample size, sampling age and location of the recent important studies on the early-life gut microbiota. Only full-term delivery (gestation age ≥ 37 weeks) cohort studies with over 20 participants are listed, with exception of the landmark study of Dominguez-Bello *et al.* (2010). 16S: 16S rRNA gene amplicon; metagenomics: whole-genome shotgun. Subject (CS): number of sequenced babies with those born via caesarean section in brackets.

1.6 Aims

The overarching hypothesis of this thesis is that perturbation events in very early life have both short-term and long-term impacts on the developmental dynamics of the gut microbiota.

Based on above-mentioned novelty and strength of the BBS dataset, this thesis aims to: 1) determine and characterise the "normal" development trajectory of the gut microbiota in very early life, and the main dominant colonisers in the absence of early-life perturbation events (Chapter 2);

2) determine and elucidate the short (neonatal period) and longer-term (infancy period) impact of putative perturbation events on the establishment and development of the early-life gut microbiota, including caesarean-section delivery and antibiotic usage (Chapter 3);

3) discover and catalogue the unknown microbial diversity in the neonatal gut microbiota (Chapter 4).

The objectives relevant to each aim are stated under the introduction of each chapter.

Chapter 2: Perturbations of the gut microbiota assembly in very early life

2.1 Introduction and aims

Recent large cohort studies (Stewart *et al.*, 2018; Vatanen *et al.,* 2018) have provided significant insights into the dominant role of breastfeeding in shaping the infant gut microbiota in the first 3 years of life. However, due to limited sample size, lack of longitudinal sampling, the poor taxonomic resolution provided by 16S rRNA gene profiling, the dynamic microbiota colonisation events during the neonatal period (0-3 weeks) remain poorly understood. This is a critical window of microbial colonisation and immune development that could impact an individual's longer-term health.

In this chapter, I assembled a UK birth cohort of 771 full-term (37-42 gestation weeks) babies and mothers and carried out whole-genome shotgun sequencing of 1,679 gut microbiotas sampled during the first three weeks of life. By performing the largest, longitudinal metagenomic characterisation of the human gut microbiota in a previously under-sampled neonatal period (≤1 month), I investigated the role of early-life events in shaping the neonatal gut microbiota composition, colonisation trajectory and the transmission of maternal microbiota in very early life.

The aims of the research presented in this chapter are to:

- Characterise the colonisation trajectory of the gut microbiota in the neonatal period, including the stability, individuality and primary colonisers of the microbiota;
- Identify the main factors and the associated bacterial taxa that affect the community composition of the neonatal gut microbiota;

- Identify and quantify the mother-to-baby bacterial transmissions at the strain level, and characterise the differences in maternal transmission pattern by birth modes.

2.2 Materials and methods

2.2.1 Study population

The study was approved by the NHS London – City and East Research Ethics Committee (REC reference 12/LO/1492). Participants were recruited at the Barking, Havering and Redbridge University Hospitals NHS Trust, the University Hospitals Leicester NHS Trust and the University College London Hospitals NHS Foundation Trust, through the BBS (previously known as Life Study enhancement pilot study) from May 2014 to December 2017. All pregnant women who arrived at the labour ward to give birth were approached for recruitment, with the exception of those under 16 years of age and non-UK residents who intended to return abroad immediately after delivery. Mothers provided written informed consent for their participation, and for the participation of their children, in the study. The study was performed in compliance with all relevant ethical regulations.

2.2.2 Sample collection

Faecal samples were collected from babies, with at least 1 sample in the first 21 days of life (primarily on day 4, 7 or 21). For a subset of babies who provided neonatal samples, a follow-up collection of a faecal sample was performed between 4 and 12 months of their lives. Maternal faecal samples were collected in the maternity unit before or after delivery, or stool was collected during delivery by midwives. Baby samples were collected at home by mothers, and returned to the processing laboratory by post at ambient temperature within 24 h. On arrival at the laboratory, all faecal samples were immediately stored at 4 °C for an average of 2.41 days (95% confidence interval 2.06–2.76 days) before further processing. Samples were aliquoted into 6 vials, 4 of which were stored at -80 °C for raw faeces biobanking; the other two vials were processed immediately for DNA extraction. This sample storage and processing protocol

was assessed during in a BBS pilot study, and was shown to be robust to technical variation in microbiome measurements at the time of study design (discussed in 2.3.8).

DNA was extracted from 30 mg of faecal samples using FastDNA Spin Kit for Soil (MP-Biomedicals, Part No. 116560200) as previously described (Bailey *et al.*, 2017). Briefly, 300µl of 100mg/ml faecal samples were spun down and re-suspended in the beads and lysis solutions. Bead beating was performed on a FastPrep-24 (MP Biomedicals, Part No. 116004500) for 10mins at 14000g, and otherwise following the manufacturer recommended protocol. Negative controls using ultrapure water were included in parallel for each kit as well as each extraction batch, and DNA concentration was quantified to confirm it was contamination-free. Total DNA was eluted in 60 µl DNase/Pyrogen-free water, and stored at -80 °C until shipment to the Wellcome Sanger Institute for metagenomic sequencing.

2.2.3 Shotgun metagenomic sequencing and analysis

DNA samples, including negative controls, were quantified by PicoGreen dsDNA assay (Thermo Fisher), and samples with >100 ng DNA material proceeded to library preparation (TruSeq DNA PCR-Free, Illumina) and paired-end (2 × 125 bp) metagenomics sequencing on the HiSeq 2500 v4 platform. Low-quality bases were trimmed (*SLIDINGWINDOW:4:20*), and reads below 87 nucleotides in length (70% of original read length) were removed (*MINLEN:87*) using Trimmomatic (Bolger *et al.*, 2014). To remove potential human contaminants, quality-trimmed reads were screened against the human genome (GRCh38) with Bowtie2 v.2.3.0 (Ben Langmead, Salzberg, 2012). On average, 22.4 (95% confidence interval 22.1–22.6) million raw reads were generated per sample. There were 19.3 (95% confidence interval 19.1–19.6) million reads (87.3% of the raw reads) per sample that passed decontamination and quality-trimming steps for downstream analysis. Sequencing depth and batch (run) were included as potential technical confounding factors in analyses of microbiota species and strain measurements, and significant species association with clinical covariates. Taxonomic classification from

metagenomics reads was performed using Kraken v.1.0 (Wood, Salzberg, 2014), a *k*-mer-based sequence classification approach against a customised database consisting of the genomes in the Human Gastrointestinal Bacteria Genome Collection (Forster *et al.*, 2019). Bracken v.1.0 (Lu *et al.*, 2017) was run on the Kraken classification output to estimate taxonomic abundance down to the species level. Metagenomic samples were compared at the genus and species levels by relative abundance. As previously described (Browne *et al.*, 2016), a cut-off of 100 Kraken-assigned paired-end reads (which corresponds to 0.001% relative abundance, given the sampling depth of about 10 million paired-end reads) was applied to determine metagenomic species detection. The R packages *phyloseq* v1.28.0 (McMurdie, Holmes, 2013) and *microbiome* v1.6.0 (Lahti, Shetty, 2017) were used for metagenomic data analysis, and results were visualised using *ggplot2* (Wickham, 2016) in RStudio.

2.2.4 Classification of babies with the low-*Bacteroides* profile

For each baby, the median relative abundance of the *Bacteroides* genus was calculated across samples from the neonatal period. On the basis of the previously described threshold (Yassour *et al.*, 2016), babies with a median abundance of less than 0.1% were assigned the low-*Bacteroides* profile.

2.2.5 Analysis of transmission of maternal microbial strains

Strain transmissions in mother–baby paired samples were determined using a single-nucleotide-variant-calling method (Truong *et al.*, 2017). StrainPhlAn v1.0 was run on pre-processed metagenomes to generate consensus species-specific marker genes for phylogenetic reconstruction of all detectable strains (one dominant strain per sample), using default parameters and with the options '*–alignment_program mafft*' and '*–relaxed_parameters3*', as previously described (Ferretti *et al.*, 2018). No significant variation in sequencing depth that had any effect on the coverage-dependent detection of microbiota species and strains was observed between babies delivered vaginally or by caesarean section, across age groups

(discussed in 2.3.7). For each species and strain with sufficient coverage (greater than 1x as per StrainPhlAn's default parameter) for strain profiling, I generated a species-specific phylogenetic tree using RAxML (Stamatakis, 2014). As previously described (Ferretti *et al.*, 2018), the strain distance for each pair of mother–baby sample strains was computed by calculating the pairwise normalised phylogenetic distance on the corresponding species tree.

To define strain-transmission events, a previously described (Ferretti *et al.*, 2018) conservative threshold of 0.1 on the strain distance value was used. The detectable strains in a given pair of mother–baby samples were considered to be identical (strain distance of less than 0.1, indicating transmission) or distinct (a strain distance of greater than 0.1, indicating no transmission). For all mother–baby pairs shown in Figure 2.12, an early transmission event was counted once per species per mother–baby pair, considering the detected transmission (or evidence for no transmission) at the earliest time point (primary transmission), irrespective of the subsequent transmission events in any later neonatal-period samples. For a subset of mother–baby pairs with both neonatal- and infancy-period sampled (Figure 2.13), late transmission events were counted separately, including cases of no early transmission owing to insufficient coverage (no detectable strains). To highlight the transmission pattern shared by phylogenetically related species, a neighbour-joining (Gascuel, 1997) tree of the eligible species was constructed on the basis of the mash distance matrix (Ondov *et al.*, 2016) of the respective reference genomes included in the StrainPhlAn database (Appendix 1). The same approach and strain-distance threshold (core-genome single-nucleotide polymorphisms (SNPs)) were applied to the cultured strains to count the number of identical and distinct strains within mother–baby and longitudinal paired samples.

2.2.6 Statistical analysis

To calculate the effect of clinical covariates on the composition of the gut microbiota, I stratified by age groups and then assessed the proportion of explained variance (R^2 from PERMANOVA) in Bray–Curtis dissimilarity for each clinical covariate, using the *adonis* function from the R

package *vegan* (Oksanen *et al.*, 2014). PERMANOVA is mostly unaffected by group dispersion effects in balanced designs (Anderson, Walsh, 2013), such as comparisons between mode of delivery); for unbalanced designs (such as breastfeeding comparisons) that are more sensitive to group dispersion effects, the group variance homogeneity condition was validated using the *betadisper* function. Group dispersions were not significantly different (*betadisper,* $P < 0.05$) in all comparisons, which lent support to the significant - albeit visibly weak - effects of breastfeeding as reported by PERMANOVA. Samples with missing metadata for the given clinical covariate were excluded before running each cross-sectional analysis. Effect sizes and statistical significance were determined by 1,000 permutations, and *P* values were corrected for multiple testing using the Benjamini–Hochberg false-discovery rate (of 5%). Statistical tests of between-group comparisons of taxonomic abundance (Welch's *t*-test with false-discovery-rate-corrected *P* values) were performed in the Statistical Analysis of Metagenomics Profiles (STAMP) program v.2.0 (Parks *et al.*, 2014). MaAsLin (Morgan *et al.*, 2012) was used for the adjustment of covariates when determining the significance of species associated with a specific variable, while accounting for potentially confounding covariates, as previously described (Stewart *et al.*, 2018; Vatanen *et al.,* 2018). All the covariates that were tested in the PERMANOVA were included in the adjustment, along with the sequencing depth used as a fixed effect. The default MaAsLin parameters were applied (maximum percentage of samples with missing metadata of 10%, minimum percentage relative abundance of 0.01%, $P < 0.05$, $q < 0.25$).

2.2.7 Data availability

The metagenomic sequencing data generated and analysed in this study have been deposited in the European Nucleotide Archive under accession numbers ERP115334. The raw faecal samples and clinical metadata are available from the Lawley Lab upon request.

2.3 Results and discussion

2.3.1 Longitudinal metagenomic sampling of the neonatal gut microbiota.

To characterise the trajectory of gut microbiota acquisition and development during the neonatal period, 596 healthy, term babies (39.5 ± 1.37 gestation weeks, 314 vaginal and 282 caesarean-section births, Figure 2.1, Table 2.1) delivered at the participating UK hospitals were enrolled through the Baby Biome Study (BBS). Faecal samples were collected in the neonatal period, primarily at day 4, 7 and 21 of age (average ~2 samples per baby). To follow the gut microbiota colonisation trajectory beyond very early life, 302 babies were resampled later, during infancy (8.75 ± 1.98 months). On average, 82.32% of the babies were breastfed during the neonatal period (day 4-21) and 87.22% were at least partially breastfed when they were sampled in infancy, and this pattern did not vary between modes of delivery (age group-paired Wilcoxon test, $p = 0.375$). To investigate the transmission of maternal microbiota, faecal samples were also obtained from 175 mothers paired with 179 babies (including 4 twins).

Having assembled this large UK microbiome cohort during the first half of my project, I then proceeded to perform whole-genome shotgun metagenomic sequencing on 1,679 faecal samples from a total of 771 babies and mothers, generating a combined 2.7 terabytes of sequencing data (average 22.2 million raw reads per sample). Whilst previous cohorts heavily skewed towards sampling vaginal births, the BBS cohort is well-balanced with respect to the mode of delivery (47.3% caesarean section) and infant gender (48.4% female), which had provided sufficient statistical power to detect significant differences in the gut microbiota composition, colonisation trajectory and maternal transmission pattern by modes of delivery.

Overall, the BBS dataset represents the largest, longitudinal shotgun metagenomic characterisation of the human gut microbiota during an under-sampled neonatal period, which more than tripled the sample size of the largest comparable public dataset ($n = 98$, Bäckhed *et al.*, 2015).

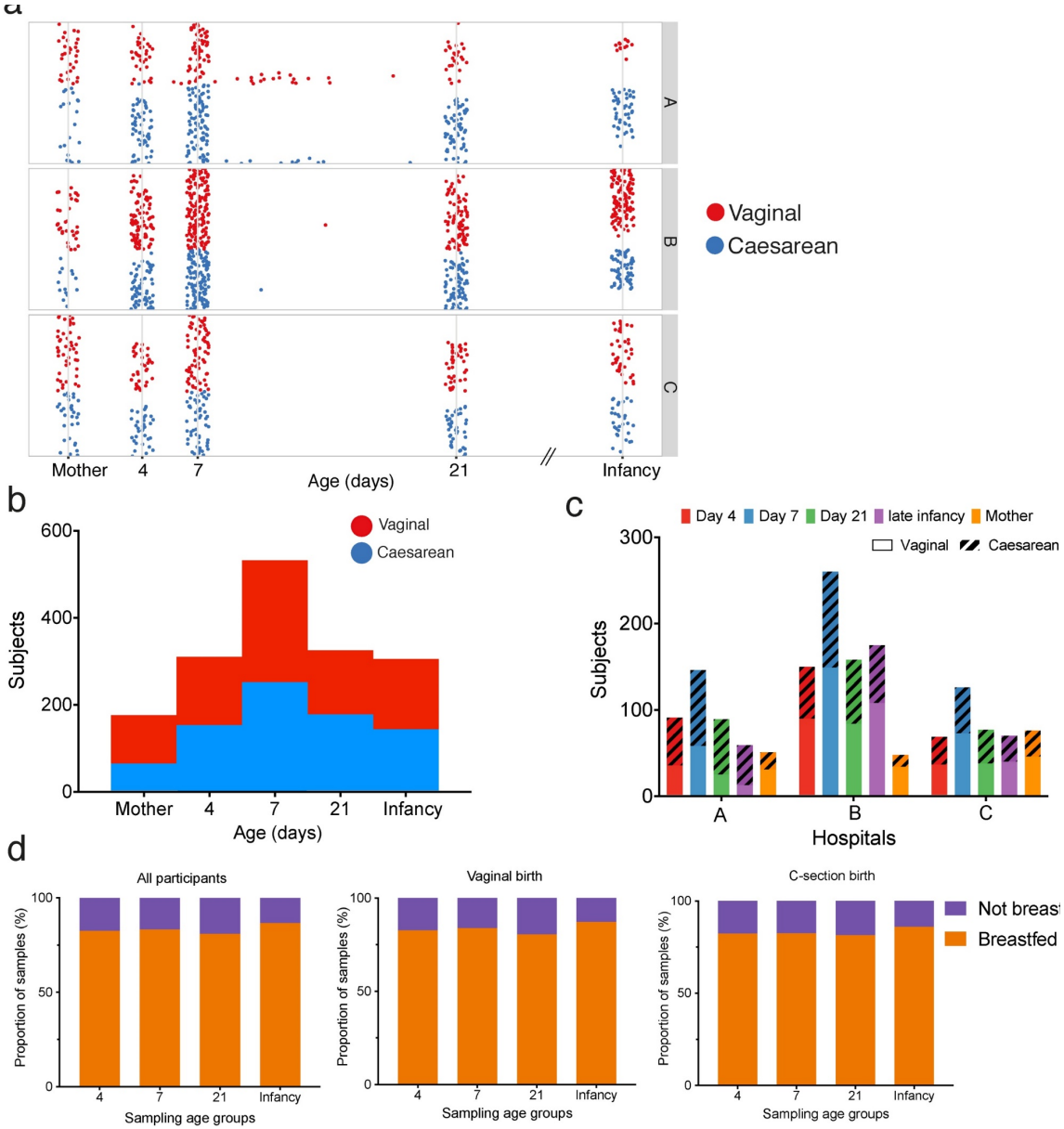

Figure 2.1 Longitudinal sampling of 1,679 gut metagenomes in the Baby Biome Study.

a, Longitudinal metagenomic sampling of 1,679 gut microbiotas, from 771 Baby Biome study (BBS) participants recruited at three UK NHS hospitals (labelled A, B and C) in Leicester and London. Each row corresponds to the time course of a subject. Five hundred and ninety-six babies were sampled during the neonatal period, primarily on day 4 ($n = 310$), day 7 ($n = 532$) and day 21 ($n = 325$), and in infancy (8.75 ± 1.98 months of age, $n = 302$), as well as 175 matched mothers. **b-d,** Summary of the metagenomic samples used for analysis in this study, across age points (**b**), hospitals (**c**) and breastfeeding status (**d**). Around half of the total samples originated from caesarean section babies (hatch pattern, vaginal/caesarean section mean ratio=1.17, s.d.=0.34, one-sample t-test to a hypothetical mean of 1, p = 0.33).

Sampling age group (subjects)	
All babies	596
Day 4	310
Day 7	532
Day 21	325
Infancy	302
Mother	175
Mode of delivery – Caesarean section	
All babies	282 (47.3%)
Day 4	153 (49.4%)
Day 7	252 (47.4%)
Day 21	178 (54.8%)
Infancy	142 (47.0%)
Mother	65 (37.1%)
Mode of feeding – Non-breastfeeding	
Day 4	52 (17.5%)
Day 7	83 (16.8%)
Day 21	59 (19.0%)
Infancy	33 (13.4%)
Antibiotics	
Intrapartum antibiotic prophylaxis (vaginal delivery)	23 (7.3%)

Table 2.1 The main clinical characteristics of the BBS cohort.

The spreadsheet containing the complete clinical metadata of 1,679 study participants analysed in this study is attached as Appendix 2. A total of 233 babies have longitudinally sampled across all major time points (day 4, 7 and 21) in the neonatal period, of which 97 babies were subsequently sampled when they progressed into infancy"

2.3.2 Neonatal gut microbiota exhibits high volatility and individuality.

Reference genome-based (Forster *et al.*, 2018) metagenomic analysis of the 1,679 faecal samples taken in total allowed determination of species and strain-level composition. This demonstrated the age-dependent, temporal shifts in the gut microbiota composition as measured by beta-diversity (Figure 2.2a), as well as increased microbiota species richness (measured by alpha diversity) over developmental time (Figure 2.2b).

To assess the stability of the neonatal gut microbiota, I investigated the intra and inter-individual microbiota differences in babies longitudinally sampled through the neonatal period (two windows of day 4 to 7, day 7 to 21). Between individuals, the neonatal gut microbiota exhibited substantial heterogeneity (Figure 2.2c), which was substantially higher in comparison to the TEDDY study babies measured from 3 months of age (Vatanen *et al.*, 2018), and adult represented by the maternal samples (Figure 2.2d). Within individual babies, the gut microbiota showed substantial instability (intra-individual variability) during the first three weeks of life (Figure 2.2c), in comparison to the stability level measured at and from 3 months of age in the TEDDY study (Vatanen *et al.*, 2018).

Indeed, inter-individual differences explained 57% of the variation in microbial species composition (permutational multivariate analysis of variance (PERMANOVA), $P < 0.001$, 1,000 permutations); this was followed by age at sampling, which explained 5.7% of the variance ($P < 0.001$). Taken together, these results highlight that the human gut microbiota is highly unstable and individualised during the neonatal period, much more so than was previously observed during infancy, and in adults, indicating that the initial colonisation process in the gut microbiota is very dynamic.

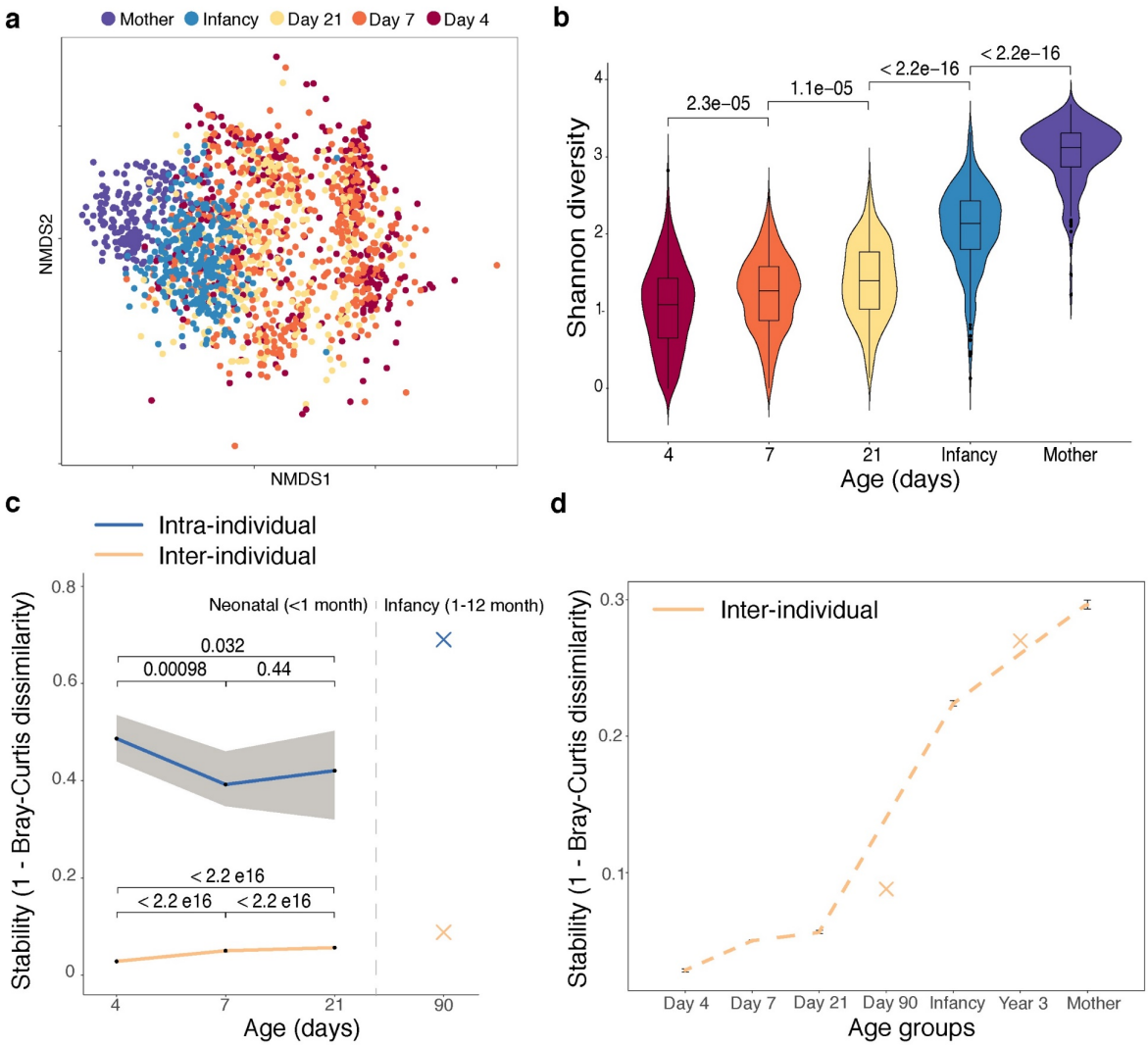

Figure 2.2 Developmental dynamics of the neonatal gut microbiota.

a, Nonmetric multidimensional scaling (NMDS) ordination of bacterial beta-diversities, measured by Bray–Curtis dissimilarity between species relative abundance profiles (n = 1,679 samples). **b-d,** Neonatal gut microbiota exhibits high volatility and individuality. Microbiota alpha diversity (Shannon diversity index) increased over developmental time (**b**). The violin plot outlines the kernel probability density; the width of the shaded area represents the proportion of the data shown. Centre line shows median; box limits indicate the 25th and 75th percentiles; whiskers extend 1.5× the interquartile range from the 25th and 75th percentiles, and outliers are represented by dots. The gut microbiota of neonates on day 4 (n = 310 individuals), 7 (n = 532 individuals) and 21 (n = 325 individuals), and in infancy (n = 302 individuals), as well as from matched mothers (n = 175), are plotted. **c**, **d**, Stability of the gut microbiota, stratified by inter-individual (day 4, n = 310 individuals; day 7, n = 532 individuals; and day 21, n = 325 individuals) and intra-individual comparisons in sliding time windows (day 4 to 7, n = 274 individuals and day 7 to 21, n = 285 individuals) during the neonatal period (**c**), in the context of the overall infancy period (**d**). Microbiota stability measurements from the TEDDY study (the earliest measurements on day 90, and at year 3, Vatanen *et al.*, 2018), are plotted in crosses. Solid lines show the median per time window. Shaded areas show the 99% confidence interval, estimated using binomial distribution. Error bars indicate median absolute deviation. Significance between groups was determined by two-sided Wilcoxon rank-sum test.

2.3.3 Mode of delivery drives gut microbiota colonisation in very early life.

To determine the effect of clinical covariates on the composition of the gut microbiota, I performed cross-sectional PERMANOVA and stratified by age. The mode of delivery was the most significant factor to drive variation in the gut microbiota during the neonatal period (Figure 2.3, Table 2.2). Breastfeeding (discussed in the section 2.3.4), as well as clinical covariates that are associated with hospital births (such as the use of perinatal antibiotics and the duration of the stay in hospital), exhibited smaller effects. The largest effect of the mode of delivery was observed on day 4 ($R^2 = 7.64\%$, $P < 0.001$, Figure 2.4a-d); this effect dissipated with age but remained significant at the point of sampling in infancy ($R^2 = 1.00\%$, $P = 0.002$).

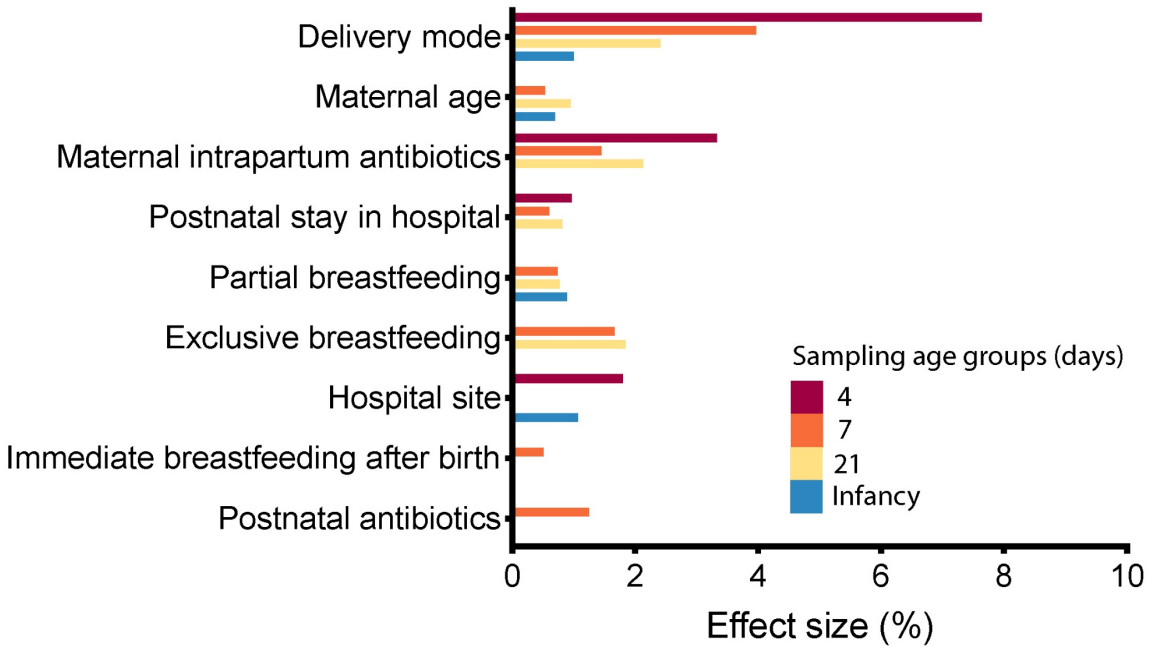

Figure 2.3 Gut microbiota variation associated with early-life clinical covariates.

Bar plot illustrating the clinical covariates that are associated with variation in the neonatal-gut microbiota on day 4 ($n = 310$ individuals), day 7 ($n = 532$ individuals), day 21 ($n = 325$ individuals) and in infancy ($n = 302$ individuals). Only significant associations in cross-sectional tests are shown. Covariates are ranked by the number of significant effects observed across sampling-age groups. The effect size (proportion of explained variance R^2) and significance were determined by PERMANOVA on between-sample Bray–Curtis dissimilarity (Table 2.2).

Whilst previous studies suggested that the neonatal (meconium at birth, Chu *et al.*, 2017) and infant (4-month-old (Azad *et al.*, 2013) gut microbiota could differ according to the indications of caesarean section (emergency, typically laboured or elective, typically unlaboured), here I observed no differences between maternal gut microbiota by mode of delivery (Figure 2.4e), or between neonatal gut microbiotas by types of caesarean-section birth (elective versus emergency, Table 2.2).

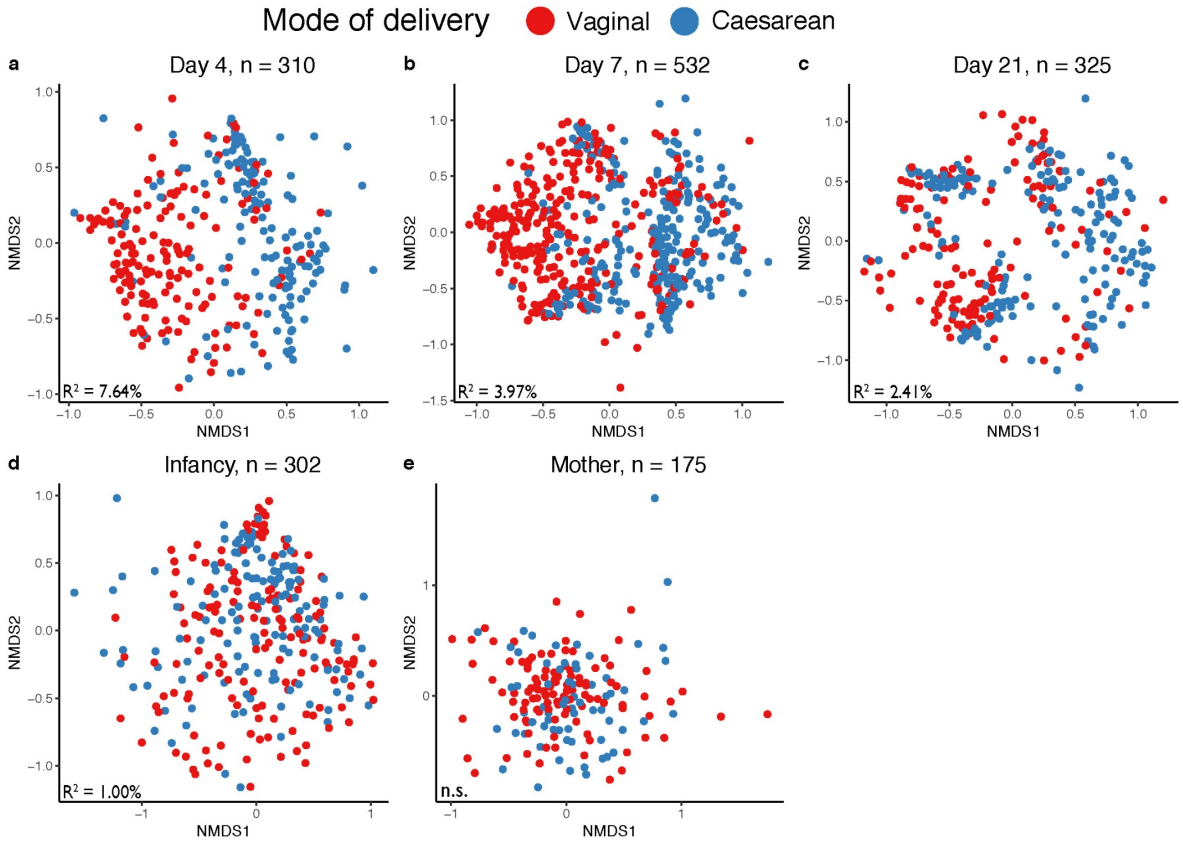

Figure 2.4 Microbiota variation associated with the mode of delivery in the neonatal period and infancy.

a-e, Non-metric multidimensional scaling ordination of Bray–Curtis dissimilarity between the species relative-abundance profiles of the gut microbiota sampled from babies on day 4 (**a,** vaginally delivered, $n = 157$ babies; delivered by caesarean section, $n = 153$ babies), day 7 (**b,** vaginally delivered, $n = 280$ babies; delivered by caesarean section, $n = 252$ babies), day 21 (**c,** vaginally delivered, $n = 147$ babies; delivered by caesarean section, $n = 178$ babies), during infancy (**d,** vaginally delivered, $n = 160$ babies; delivered by caesarean section, $n = 142$ babies) and from mothers (**e,** $n = 110$ mothers who delivered vaginally; $n = 65$ mothers who delivered via caesarean section). The microbial variation explained by the mode of delivery is represented by the PERMANOVA R^2 value (bottom left), and is significant across four cross-sectional PERMANOVA tests. False-discovery-rate-corrected P values are reported in Table 2.2).

Table 2.2 PERMANOVA result for all study subjects.

Variance of species taxonomic profiles (Bray-Curtis distances) explained by each clinical covariate in cross-sectional PERMANOVA of all subjects, and stratified by vaginal and caesarean-section deliveries. Tables contain R-squared (the proportion of variance explained), nominal p-value based on 1,000 permutation tests (two-sided), and FDR-adjusted p-values (q-values) after multiple comparisons (Benjamini-Hochberg false discovery rate = 5%) for each covariate in cross-sectional PERMANOVA. Empty cells indicate groups with insufficient metadata to perform

Covariates	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA
Mode of delivery	7.642%	0.0010	0.0035	310	3.972%	0.0010	0.0035	532	2.408%	0.0010	0.0047	325	1.004%	0.0020	0.0240	302	0.741%	0.1459	0.3404333	175
Hospital site	1.798%	0.0010	0.0035	310	0.509%	0.1279	0.1628	532	0.850%	0.1189	0.1665	325	1.074%	0.0080	0.0390	302	1.721%	0.0170	0.119	175
Breastfeeding ongoing	0.652%	0.0270	0.0747	297	0.742%	0.0010	0.0035	494	0.777%	0.0090	0.0210	310	0.894%	0.0130	0.0390	247	-	-	-	-
Exclusive breastfeeding	1.083%	0.0320	0.0747	297	1.691%	0.0010	0.0035	494	1.868%	0.0020	0.0070	310	-	-	-	-	-	-	-	-
Gender	0.283%	0.6184	0.6184	295	0.227%	0.2967	0.3462	489	0.241%	0.7003	0.7003	315	0.575%	0.0460	0.0920	300	0.516%	0.8871	0.8871	160
Maternal age	0.518%	0.1798	0.2288	260	0.572%	0.0030	0.0070	441	0.991%	0.0030	0.0084	277	0.738%	0.0120	0.0390	286	0.711%	0.3337	0.583975	150
Days in hospital	0.971%	0.0010	0.0035	295	0.597%	0.0020	0.0056	489	0.823%	0.0010	0.0047	315	0.490%	0.0749	0.1284	301	0.899%	0.1269	0.3404333	160
Hopspital_destination_room_risk	0.412%	0.2917	0.3403	284	0.341%	0.0699	0.0979	475	0.537%	0.0699	0.1398	309	0.705%	0.0220	0.0528	298	-	-	-	-
Birth weight	0.482%	0.1249	0.1943	296	0.387%	0.0360	0.0560	489	0.426%	0.1898	0.2416	316	0.382%	0.2817	0.3756	300	-	-	-	-
Breastfed_with_1hr_birth	0.572%	0.0779	0.1363	281	0.511%	0.0040	0.0080	473	0.534%	0.0799	0.1398	306	0.197%	0.8511	0.8511	297	-	-	-	-
Abx_mother_prior_birth	0.796%	0.1698	0.2288	310	0.388%	0.4126	0.4126	532	0.825%	0.0899	0.1398	325	-	-	-	302	0.931%	0.8741	0.8871	175
Abx_mother_birth_IAP	3.334%	0.0010	0.0035	189	1.445%	0.0010	0.0035	308	2.134%	0.0010	0.0047	217	0.673%	0.3327	0.3992	167	1.492%	0.8342	0.8871	96
Abx_mother_after_hospital	0.937%	0.5135	0.5530	310	0.391%	0.4076	0.4126	532	0.609%	0.4805	0.5175	325	0.265%	0.5904	0.6441	302	-	-	-	-
Abx_baby_postnatal	2.938%	0.0510	0.1020	63	1.252%	0.0080	0.0140	187	1.153%	0.3467	0.4045	96	1.700%	0.2488	0.3732	73	-	-	-	-

Table 2.3 PERMANOVA result for caesarean-section delivery subjects.

Variance of species taxonomic profiles (Bray-Curtis distances) explained by each clinical covariate in cross-sectional PERMANOVA of caesarean-section delivery subjects, and stratified by vaginal and caesarean-section deliveries. Tables contain R-squared (the proportion of variance explained), nominal p-value based on 1,000 permutation tests (two-sided), and FDR-adjusted p-values (q-values) after multiple comparisons (Benjamini-Hochberg false discovery rate = 5%) for each covariate in cross-sectional PERMANOVA. Empty cells indicate groups

Covariates	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA
Mode of delivery	-	-		-	-	-	-		-	-	-		-	-	-	-
Hospital site	2.934%	0.0020	0.0260	153	0.574%	0.8741	0.9391	252	1.012%	0.6194	0.7035	178	1.445%	0.4206	0.6835	142	3.550%	0.2228	0.5570	65
Breastfeeding ongoing	1.469%	0.0260	0.0845	147	1.176%	0.0020	0.0130	240	0.916%	0.1009	0.2143	172	0.559%	0.8631	0.9631	114	-	-	-	-
Exclusive breastfeeding	2.969%	0.0150	0.0845	147	2.392%	0.0010	0.0130	240	2.484%	0.0130	0.1560	172	3.934%	0.8890	0.9631	114	-	-	-	-
Gender	0.584%	0.5880	0.7644	145	0.860%	0.0280	0.1213	234	0.538%	0.4950	0.7035	172	1.168%	0.0670	0.2903	140	1.442%	0.7153	0.7153	60
Maternal age	1.137%	0.1479	0.3205	127	0.548%	0.3097	0.4965	212	1.288%	0.0240	0.1560	153	1.068%	0.1399	0.4547	132	1.763%	0.4126	0.6656	59
Days in hospital	0.360%	0.9061	0.9491	145	0.534%	0.1888	0.4437	235	0.854%	0.0510	0.1635	173	0.637%	0.5425	0.7118	141	1.607%	0.5325	0.6656	60
Hopsital_destination_room_risk	1.130%	0.0909	0.2363	140	0.474%	0.3367	0.4965	229	0.968%	0.0629	0.1635	169	1.848%	0.0030	0.0390	141	-	-	-	-
Birth weight	0.782%	0.9491	0.9491	146	0.547%	0.2048	0.4437	236	0.522%	0.5664	0.7035	173	0.634%	0.5475	0.7118	142	-	-	-	-
Breastfed_with_1hr_birth	0.320%	0.8282	0.9491	140	0.239%	0.9391	0.9391	229	0.283%	0.9441	0.9441	168	0.340%	0.9650	0.9650	140	-	-	-	-
Abx_mother_prior_birth	1.932%	0.5145	0.7432	153	0.791%	0.4715	0.5572	252	1.478%	0.1299	0.2143	178	0.799%	0.3117	0.6754	142	-	-	-	-
Abx_mother_birth_IAP	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Abx_mother_after_hospital	1.932%	0.4825	0.7432	153	0.791%	0.4675	0.5572	252	1.478%	0.1319	0.2143	178	0.799%	0.3047	0.6754	142	-	-	-	-

Table 2.4 PERMANOVA result for vaginal delivery subjects.

Variance of species taxonomic profiles (Bray-Curtis distances) explained by each clinical covariate in cross-sectional PERMANOVA of vaginal delivery subjects, and stratified by vaginal and caesarean-section deliveries. Tables contain R-squared (the proportion of variance explained), p p p p
Hochberg false discovery rate = 5%) for each covariate in cross-sectional PERMANOVA. Empty cells indicate groups with insufficient p

Covariates	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA	R2	p-value	q-value	N.not.NA
Mode of delivery	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Hospital site	2.447%	0.0090	0.0563	157	1.522%	0.0070	0.0152	280	2.180%	0.0629	0.1152	147	1.282%	0.4086	0.7005	160	2.709%	0.0290	0.0870	111
Breastfeeding ongoing	0.913%	0.1788	0.3874	150	0.997%	0.0070	0.0152	254	1.445%	0.0330	0.0936	138	2.338%	0.0040	0.0480	133	-	-	-	-
Exclusive breastfeeding	1.101%	0.3606	0.5860	150	2.171%	0.0050	0.0152	254	2.433%	0.0360	0.0936	138	-	-	-	-	-	-	-	-
Gender	0.261%	0.9720	0.9720	150	0.210%	0.8931	0.8931	255	0.308%	0.9610	0.9610	143	1.150%	0.0330	0.0990	160	0.949%	0.5275	0.6510	101
Maternal age	0.694%	0.5185	0.7489	133	0.522%	0.2478	0.3221	229	1.122%	0.1708	0.2220	124	0.912%	0.1469	0.2938	154	1.058%	0.4755	0.6510	92
Days in hospital	1.437%	0.0130	0.0563	150	1.328%	0.0030	0.0130	254	1.822%	0.0060	0.0390	142	1.177%	0.0260	0.0990	160	1.786%	0.0210	0.0870	101
Hopspital_destination_room_risk	0.599%	0.5844	0.7597	144	0.825%	0.0440	0.0715	246	1.139%	0.1169	0.1689	140	1.225%	0.0230	0.0990	157	-	-	-	-
Birth weight	1.420%	0.0230	0.0748	150	0.770%	0.0370	0.0687	253	1.529%	0.0190	0.0823	143	1.133%	0.0530	0.1272	158	-	-	-	-
Breastfed_with_1hr_birth	0.447%	0.8282	0.9720	141	0.345%	0.5914	0.6407	244	1.313%	0.0679	0.1152	138	0.395%	0.8561	0.8561	157	-	-	-	-
Abx_mother_prior_birth	0.790%	0.9341	0.9720	157	0.752%	0.3866	0.4569	280	1.883%	0.0709	0.1152	147	0.559%	0.6284	0.8561	160	1.718%	0.5425	0.6510	111
Abx_mother_birth_IAP	13.612%	0.0010	0.0130	36	5.876%	0.0010	0.0130	56	12.487%	0.0010	0.0130	39	3.601%	0.6723	0.8561	25	4.693%	0.9371	0.9371	32
Abx_mother_after_hospital	1.684%	0.1179	0.3065	157	0.855%	0.2408	0.3221	280	1.447%	0.3726	0.4091	147	0.411%	0.8332	0.8561	160	-	-	-	-
Abx_baby_postnatal	3.571%	0.2238	0.4156	37	2.685%	0.0030	0.0130	104	2.319%	0.3776	0.4091	30	1.531%	0.8551	0.8561	42	-	-	-	-

Given the significant effect of the mode of delivery during the neonatal period, I next sought to understand how the composition and developmental trajectory of the microbiota were altered. To identify the bacterial species and genera present at the differential abundance in gut microbiota samples by different modes of delivery, I stratified samples by age groups and performed univariate (Figure 2.5, Figure 2.6) statistical tests for significantly differential species and genera associated with mode of delivery. Samples from babies delivered vaginally were enriched with species of *Bifidobacterium* (such as *Bifidobacterium longum* and *Bifidobacterium breve*), *Escherichia* (*Escherichia coli*), *Bacteroides* (*Bacteroides vulgatus*) and *Parabacteroides* (*Parabacteroides distasonis*), and these commensal genera comprised 68.3% (95% confidence interval, 65.7–71.0%) of the neonatal gut microbiota (Figure 2.7), consistent with recent observations in other birth cohorts (Bäckhed *et al.*, 2015; Wampach *et al.*, 2018). By contrast, the gut microbiota of babies delivered by caesarean section were depleted of these commensal genera and instead were dominated by *Enterococcus faecalis*, *Enterococcus faecium*, *Staphylococcus epidermis*, *Streptococcus parasanguinis*, *Klebsiella oxytoca, Klebsiella pneumoniae*, *Enterobacter cloacae* and *Clostridium perfringens*, all of which commonly associated with hospital environments (Lax *et al.*, 2017) and hospitalised preterm babies (Stewart *et al.*, 2015; Gibson *et al.*, 2016; Raveh-Sadka *et al.*, 2016). Importantly, all above-mentioned species except *E. coli*, *S. epidermis* and *Streptococcus* spp. were significantly associated with the mode of delivery, after statistical adjustment for potentially confounding covariates using a multivariate statistical test (Table 2.5). On day 4, species that belong to these genera accounted for 68.25% (95% confidence interval, 62.74–73.75%) of the total composition of the microbiota in babies delivered by caesarean section (Figure 2.7). Longitudinally, the relative abundance of these predominantly facultative anaerobes gradually declined through the later neonatal period and towards infancy, which coincided with the expansion of strict anaerobes *Bifidobacterium* and *Bacteroides* species in line with previous observations over this period in other cohorts (Bäckhed *et al.*, 2015; Bokulich *et al.*, 2016).

Collectively, these results highlighted the dominant role of delivery mode with associated species driving gut microbiota colonisation in the under-studied, earliest stage of human development, and a delayed commensal microbiota colonisation trajectory following caesarean-section births.

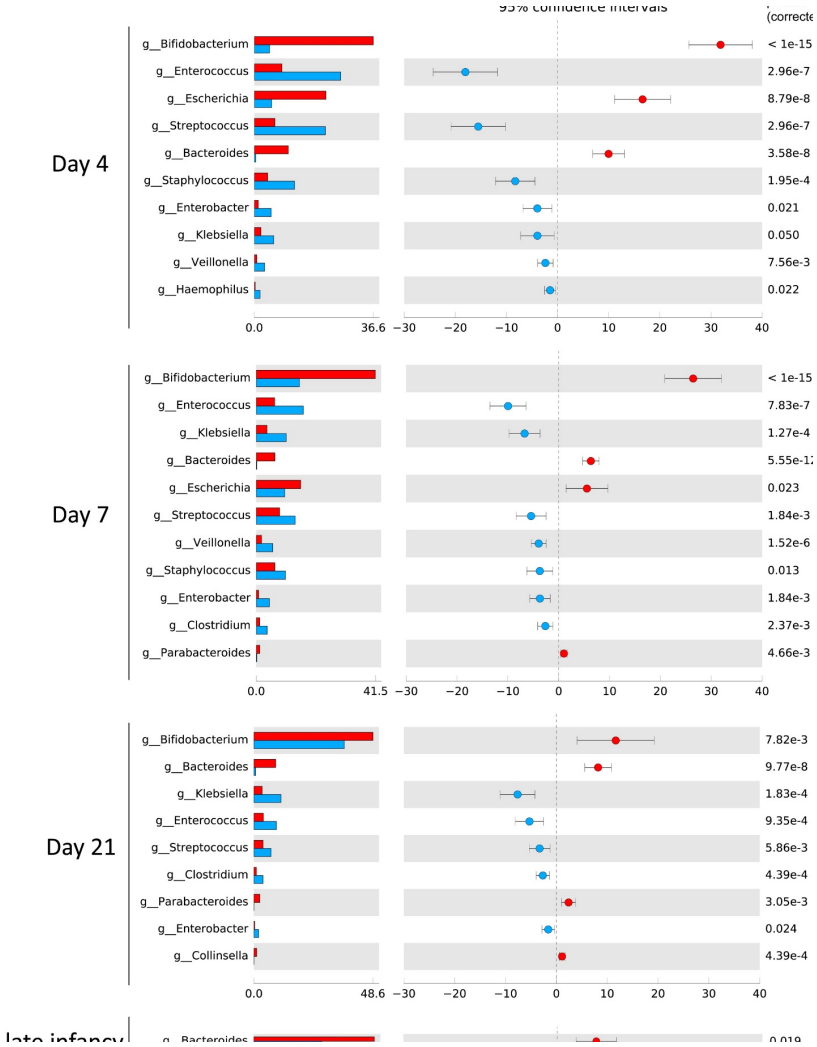

Figure 2.5 Bacterial genera with differential abundance between the modes of delivery.

a, Bacterial genera with statistically different relative abundance level of the gut microbiota of babies delivered vaginally (red) or via caesarean section (blue) in four age groups. Day 4 (vaginal, *n* = 157; caesarean section, *n* = 153), day 7 (vaginal, *n* = 280; caesarean section, *n* = 253), day 21 (vaginal, *n* = 147; caesarean section, *n* = 177), and in late infancy (vaginal, *n* = 160; caesarean section, *n* = 142). Only the genera with >1% relative abundance difference are shown. Welch's t-test was performed with p-values FDR-corrected. Error bars represent 95% confidence interval of the difference mean relative abundances. No differential genus was detected between mothers grouped by modes of delivery.

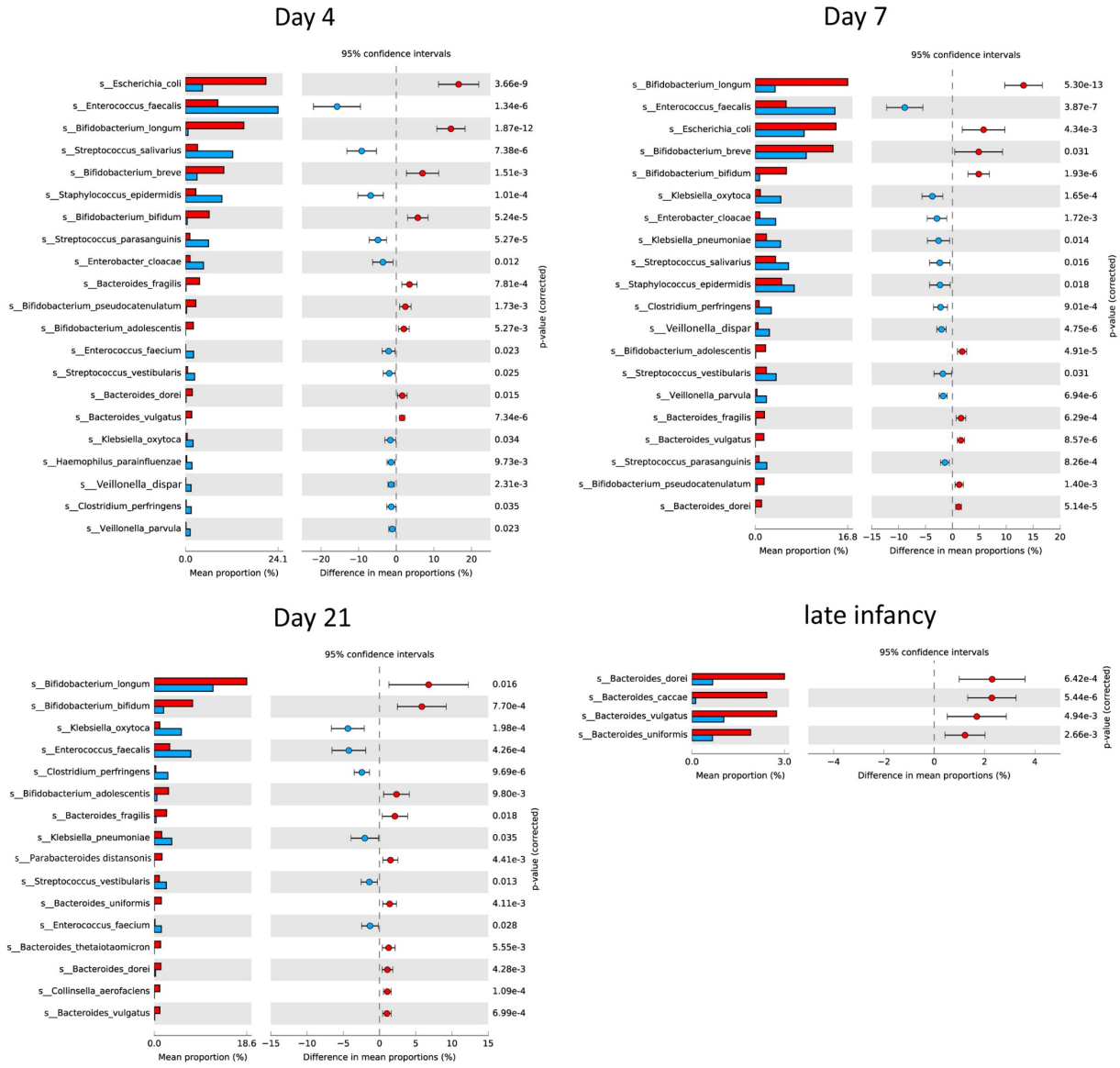

Figure 2.6 Bacterial species with differential abundance between the modes of delivery.

Bacterial species with statistically different ($p < 0.05$) abundance level of the gut microbiota of babies delivered vaginally (red) or via caesarean section (blue) in four age groups. Day 4 (vaginal, $n = 157$; caesarean section, $n = 153$), day 7 (vaginal, $n = 280$; caesarean section, $n = 253$), day 21 (vaginal, $n = 147$; caesarean section, $n = 177$), and in late infancy (vaginal, $n = 160$; caesarean section, $n = 142$). Only the genera with >1% relative abundance difference are shown. Welch's t-test was performed with p-values FDR-corrected. Error bars represent 95% confidence interval of the difference mean relative abundances. No differential genus was detected between mothers grouped by modes of delivery.

Table 2.5 Species associated with clinical covariates in multivariate statistical analysis.

Species associated with clinical covariates in each sampling age group, after accounting for potentially confounding covariate with MaAsLin; The opportunistic pathogen species are highlighted in red. Variable: indicated the direction together with the sign of the effect size; Effect size: the fixed effect coefficient (obtained from the linear model) of the effect for the given outcome; N: number of samples used in this comparison; N > 0: number of non-NA samples used in this comparison; p-value: nominal p-value (two-sided) for the given association; q-value: FDR corrected p-value, q-value, for the given association.

Age group	Variable	Value	Species	Effect size	N	N.not.NA	p-value	q-value
Day 4	Abx_mother_labour_IAP	No	*Bifidobacterium bifidum*	-0.5296448	310	51	0.00800413	0.15493899
Day 4	Abx_mother_labour_IAP	No	*Bifidobacterium breve*	0.00648245	310	125	0.01533722	0.24240282
Day 4	Abx_mother_prior_birth	Yes	*Escherichia coli*	0.62902174	310	162	0.002175	0.02848752
Day 4	Breastfeeding_status	Yes	*Bifidobacterium bifidum*	-0.0638664	310	51	0.02764737	0.22394368
Day 4	Breastfeeding_status	Yes	***Clostridium perfringens***	-0.0485022	310	44	0.0009727	0.01575775
Day 4	Breastfeeding_status	Yes	*Streptococcus thermophilus*	-0.0219274	310	74	2.29E-09	2.47E-07
Day 4	Breastfeeding_status	Yes	*Staphylococcus lugdunensis*	0.01743651	310	62	0.02489438	0.20941199
Day 4	Breastfeeding_status	Yes	*Haemophilus parainfluenzae*	0.03445923	310	117	0.0217713	0.19594167
Day 4	Breastfeeding_status	Yes	*Staphylococcus epidermidis*	0.0584289	310	254	0.00556945	0.06444647
Day 4	Days_in_hospital	continous variable	*Bifidobacterium longum*	-0.0623678	310	148	2.06E-05	0.00066897
Day 4	Days_in_hospital	continous variable	*Staphylococcus hominis*	-0.0095052	310	112	0.01422197	0.14399745
Day 4	Days_in_hospital	continous variable	*Streptococcus vestibularis*	-0.0007594	310	117	0.01625903	0.15493899
Day 4	Days_in_hospital	continous variable	*Bifidobacterium breve*	-0.0004442	310	125	0.00219811	0.02848752
Day 4	Days_in_hospital	continous variable	*Staphylococcus haemolyticus*	0.01628121	310	69	0.01189854	0.1285042
Day 4	Delivery_mode	Vaginal	***Enterococcus faecalis***	-0.2118591	310	196	4.85E-05	0.00131014
Day 4	Delivery_mode	Vaginal	***Enterobacter cloacae***	-0.0619815	310	73	0.00431517	0.05377371
Day 4	Delivery_mode	Vaginal	*Haemophilus parainfluenzae*	-0.0464616	310	117	8.38E-05	0.00193846
Day 4	Delivery_mode	Vaginal	*Streptococcus parasanguinis*	-0.0435736	310	212	0.00123388	0.01738157
Day 4	Delivery_mode	Vaginal	*Staphylococcus epidermidis*	-0.0416675	310	254	0.01755923	0.1625483
Day 4	Delivery_mode	Vaginal	*Veillonella parvula*	-0.030147	310	85	0.00105677	0.01630448
Day 4	Delivery_mode	Vaginal	***Clostridium perfringens***	-0.0297215	310	44	0.00619495	0.06921253
Day 4	Delivery_mode	Vaginal	*Rothia mucilaginosa*	-0.0128857	310	226	5.04E-09	4.08E-07
Day 4	Delivery_mode	Vaginal	*Veillonella dispar*	-0.0098478	310	64	0.00019687	0.00375209
Day 4	Delivery_mode	Vaginal	*Parabacteroides distasonis*	0.01950774	310	46	0.025207	0.20941199
Day 4	Delivery_mode	Vaginal	*Collinsella aerofaciens*	0.02411313	310	40	1.35E-05	0.00048715
Day 4	Delivery_mode	Vaginal	*Bacteroides uniformis*	0.02862327	310	60	3.80E-05	0.00111856
Day 4	Delivery_mode	Vaginal	*Bacteroides dorei*	0.04465788	310	50	0.00014835	0.00320439
Day 4	Delivery_mode	Vaginal	*Bifidobacterium adolescentis*	0.04709041	310	45	0.00017262	0.00349549
Day 4	Delivery_mode	Vaginal	*Bacteroides vulgatus*	0.06182235	310	68	1.39E-10	2.46E-08
Day 4	Delivery_mode	Vaginal	*Bacteroides fragilis*	0.06861412	310	33	6.68E-05	0.00166566
Day 4	Delivery_mode	Vaginal	*Bifidobacterium bifidum*	0.12064362	310	51	1.41E-07	7.59E-06
Day 4	Delivery_mode	Vaginal	*Escherichia coli*	0.29545827	310	162	1.52E-10	2.46E-08
Day 4	Hospital	B	***Enterococcus faecalis***	-0.1535343	310	196	0.01137098	0.1991459
Day 4	Hospital	B	*Gemella haemolysans*	-0.0047175	310	138	0.00673706	0.14082636
Day 7	Abx_mother_labour_IAP	Yes	*Bifidobacterium longum*	-0.2504849	532	269	0.00029799	0.00463233
Day 7	Breastfeeding_status	Yes	***Klebsiella oxytoca***	-0.0480902	532	130	0.0223055	0.21795655
Day 7	Breastfeeding_status	Yes	*Streptococcus parasanguinis*	-0.0216294	532	380	0.00516018	0.06085452
Day 7	Breastfeeding_status	Yes	*Streptococcus thermophilus*	-0.0149662	532	139	1.97E-10	1.35E-08
Day 7	Breastfeeding_status	Yes	*Streptococcus vestibularis*	-0.0038614	532	268	0.01709085	0.17191386
Day 7	Breastfeeding_status	Yes	*Gemella haemolysans*	0.00247512	532	240	0.00484031	0.05912096
Day 7	Breastfeeding_status	Yes	*Streptococcus oralis*	0.00394741	532	368	0.00106716	0.01586815
Day 7	Breastfeeding_status	Yes	*Haemophilus parainfluenzae*	0.01265637	532	233	4.96E-05	0.00089314

Age group	Variable	Value	Species	Effect size	N	N.not.NA	p-value	q-value
Day 7	Breastfeeding_status	Yes	*Staphylococcus epidermidis*	0.14330409	532	473	2.59E-11	2.95E-09
Day 7	Days_in_hospital	continous variable	*Bifidobacterium bifidum*	-0.0239214	532	98	9.06E-05	0.0015487
Day 7	Days_in_hospital	continous variable	*Streptococcus oralis*	-0.0009074	532	368	0.0037195	0.04711372
Day 7	Days_in_hospital	continous variable	*Rothia mucilaginosa*	0.00102634	532	298	0.01105473	0.11456721
Day 7	Days_in_hospital	continous variable	*Streptococcus parasanguinis*	0.00516125	532	380	0.01008983	0.11002993
Day 7	Days_in_hospital	continous variable	*Staphylococcus haemolyticus*	0.01007653	532	96	0.0065445	0.07460734
Day 7	Delivery_mode	Vaginal	***Enterococcus faecalis***	-0.1675784	532	352	1.57E-12	2.68E-10
Day 7	Delivery_mode	Vaginal	***Klebsiella oxytoca***	-0.0660725	532	130	1.61E-05	0.00032402
Day 7	Delivery_mode	Vaginal	***Enterobacter cloacae***	-0.0568811	532	152	4.57E-05	0.00086902
Day 7	Delivery_mode	Vaginal	***Clostridium perfringens***	-0.0538286	532	159	3.96E-06	0.00010423
Day 7	Delivery_mode	Vaginal	***Klebsiella pneumoniae***	-0.0182554	532	129	0.0102952	0.11002993
Day 7	Delivery_mode	Vaginal	*Veillonella dispar*	-0.017354	532	178	8.88E-06	0.00020249
Day 7	Delivery_mode	Vaginal	*Haemophilus parainfluenzae*	-0.0142294	532	233	6.97E-09	3.97E-07
Day 7	Delivery_mode	Vaginal	*Veillonella atypica*	-0.0115666	532	119	0.00133916	0.01908308
Day 7	Delivery_mode	Vaginal	*Rothia mucilaginosa*	-0.004593	532	298	0.00010605	0.00172705
Day 7	Delivery_mode	Vaginal	*Parabacteroides distasonis*	0.02000179	532	74	1.18E-06	4.04E-05
Day 7	Delivery_mode	Vaginal	*Staphylococcus hominis*	0.02231134	532	251	1.50E-05	0.00032065
Day 7	Delivery_mode	Vaginal	*Collinsella aerofaciens*	0.02337916	532	57	2.17E-06	6.74E-05
Day 7	Delivery_mode	Vaginal	*Bacteroides uniformis*	0.025537	532	83	5.18E-07	1.97E-05
Day 7	Delivery_mode	Vaginal	*Bacteroides dorei*	0.03688401	532	75	4.05E-08	1.98E-06
Day 7	Delivery_mode	Vaginal	*Bacteroides vulgatus*	0.04999246	532	93	1.76E-10	1.35E-08
Day 7	Delivery_mode	Vaginal	*Bifidobacterium bifidum*	0.07933699	532	98	2.80E-06	7.97E-05
Day 7	Delivery_mode	Vaginal	*Bifidobacterium breve*	0.10735251	532	244	0.00279101	0.03671251
Day 7	Delivery_mode	Vaginal	*Escherichia coli*	0.14760387	532	273	5.24E-06	0.00012796
Day 7	Delivery_mode	Vaginal	*Bifidobacterium longum*	0.24950021	532	269	6.09E-17	2.08E-14
Day 7	Hospital	B	*Gemella haemolysans*	-0.0027035	532	240	0.00115156	0.03150655
Day 21	Abx_Baby_after_discharge	Yes	*Rothia mucilaginosa*	-0.007543	325	169	0.01800666	0.22058155
Day 21	Abx_mother_after_hospital	Yes	***Klebsiella pneumoniae***	0.20869748	325	120	2.55E-07	2.81E-05
Day 21	Abx_mother_labour_IAP	Yes	*Bifidobacterium bifidum*	-1.0427326	325	59	4.81E-06	0.00035364
Day 21	Abx_mother_labour_IAP	No	*Bifidobacterium bifidum*	-0.8694123	325	59	0.00013124	0.00680883
Day 21	Abx_mother_prior_birth	Yes	*Escherichia coli*	0.53045749	325	222	0.00779468	0.12731317
Day 21	Breastfeeding_status	Yes	***Enterococcus faecalis***	-0.0562748	325	253	0.01734168	0.22058155
Day 21	Breastfeeding_status	Yes	*Streptococcus vestibularis*	-0.0247856	325	212	0.00866644	0.1317897
Day 21	Breastfeeding_status	Yes	*Streptococcus thermophilus*	-0.014737	325	98	2.10E-07	2.81E-05
Day 21	Breastfeeding_status	Yes	*Veillonella parvula*	-0.0137439	325	219	0.00015453	0.00486781
Day 21	Breastfeeding_status	Yes	*Intestinibacter bartlettii*	-0.0093608	325	40	3.18E-05	0.00108013
Day 21	Breastfeeding_status	Yes	***Klebsiella oxytoca***	-0.0034408	325	157	0.00125431	0.02634043
Day 21	Breastfeeding_status	Yes	*Finegoldia magna*	-0.0023569	325	108	5.13E-07	3.21E-05
Day 21	Breastfeeding_status	Yes	*Streptococcus oralis*	0.00440619	325	193	0.00682039	0.11568434
Day 21	Breastfeeding_status	Yes	*Haemophilus parainfluenzae*	0.01078608	325	141	0.00040055	0.00929705
Day 21	Breastfeeding_status	Yes	*Propionibacterium avidum*	0.0298708	325	89	0.00414158	0.07610159
Day 21	Breastfeeding_status	Yes	*Staphylococcus epidermidis*	0.06130712	325	287	0.00020569	0.00566938
Day 21	Days_in_hospital	continous variable	*Staphylococcus aureus*	-0.0029497	325	137	0.01899043	0.22634535
Day 21	Delivery_mode	Vaginal	*Bifidobacterium dentium*	-0.0746462	325	66	0.01598821	0.21366058
Day 21	Delivery_mode	Vaginal	***Enterococcus faecalis***	-0.0700231	325	253	0.00069044	0.01522427
Day 21	Delivery_mode	Vaginal	***Clostridium perfringens***	-0.0532979	325	132	6.84E-11	3.01E-08
Day 21	Delivery_mode	Vaginal	***Enterococcus faecium***	-0.0296704	325	41	0.01523203	0.20991645
Day 21	Delivery_mode	Vaginal	*Streptococcus parasanguinis*	-0.0128228	325	218	0.00865505	0.1317897
Day 21	Delivery_mode	Vaginal	***Klebsiella oxytoca***	-0.0028687	325	157	0.00193736	0.03883527
Day 21	Delivery_mode	Vaginal	*Parabacteroides distasonis*	0.03084889	325	48	6.56E-07	3.21E-05
Day 21	Delivery_mode	Vaginal	*Bacteroides vulgatus*	0.03999628	325	51	5.83E-07	3.21E-05
Day 21	Delivery_mode	Vaginal	*Bacteroides dorei*	0.04303426	325	47	3.59E-06	0.00014387

Age group	Variable	Value	Species	Effect size	N	N.not.NA	p-value	q-value
Day 21	Delivery_mode	Vaginal	*Collinsella aerofaciens*	0.04330187	325	40	1.42E-08	3.13E-06
Day 21	Delivery_mode	Vaginal	*Bacteroides uniformis*	0.04576471	325	49	5.19E-07	3.21E-05
Day 21	Delivery_mode	Vaginal	*Bifidobacterium adolescentis*	0.05484237	325	42	0.00028884	0.00707647
Day 21	Delivery_mode	Vaginal	*Bifidobacterium bifidum*	0.12946978	325	59	1.69E-06	7.45E-05
Day 21	Delivery_mode	Vaginal	*Bifidobacterium longum*	0.17948087	325	207	0.00017285	0.00508184
Day 21	Gender	Male	*Staphylococcus hominis*	0.01202873	325	166	0.01799521	0.22058155
Day 21	Hospital	B	***Klebsiella pneumoniae***	-0.0701723	325	90	0.00202226	0.07610159
Day 21	Hospital	B	*Veillonella parvula*	-0.0105829	325	219	0.00292164	0.10307537
Infancy	Breastfeeding_status	Yes	*Bacteroides caccae*	-0.1039021	302	45	1.44E-07	3.75E-05
Infancy	Breastfeeding_status	Yes	*Bacteroides ovatus*	-0.0470781	302	60	0.00582315	0.12112144
Infancy	Breastfeeding_status	Yes	*Parabacteroides merdae*	-0.0450027	302	33	2.64E-05	0.00274882
Infancy	Breastfeeding_status	Yes	*Anaerostipes caccae*	-0.0194522	302	73	0.00894941	0.16047218
Infancy	Breastfeeding_status	Yes	*Clostridium symbiosum*	-0.0162582	302	60	0.00293859	0.072765
Infancy	Breastfeeding_status	Yes	*Bilophila wadsworthia*	-0.0118737	302	37	0.00044673	0.02322992
Infancy	Breastfeeding_status	Yes	*Hungatella hathewayi*	-0.0060989	302	105	0.01028493	0.16713019
Infancy	Breastfeeding_status	Yes	*Streptococcus peroris*	0.00303106	302	134	0.00978571	0.16713019
Infancy	Breastfeeding_status	Yes	*Megasphaera nov.*	0.00432061	302	96	0.0022302	0.06103702
Infancy	Delivery_mode	Vaginal	*Bacteroides thetaiotaomicron*	0.01780275	302	41	0.01411232	0.20966881
Infancy	Delivery_mode	Vaginal	*Parabacteroides merdae*	0.02027762	302	33	0.00199816	0.05772463
Infancy	Delivery_mode	Vaginal	*Parabacteroides distasonis*	0.02304587	302	58	0.0012722	0.04725318
Infancy	Delivery_mode	Vaginal	*Bacteroides uniformis*	0.04589052	302	86	2.15E-06	0.0003735
Infancy	Delivery_mode	Vaginal	*Bacteroides vulgatus*	0.05600861	302	84	9.94E-05	0.00738233
Infancy	Delivery_mode	Vaginal	*Bacteroides dorei*	0.06128771	302	62	6.15E-05	0.00533126
Infancy	Delivery_mode	Vaginal	*Bacteroides caccae*	0.06617272	302	45	5.88E-08	3.06E-05
Mother	Abx_mother_prior_birth	Yes	*Veillonella parvula*	0.02341109	175	78	1.24E-06	0.0013748
Mother	Hospital	B	*Bifidobacterium animalis*	-0.0110635	175	49	0.00014586	0.1620481

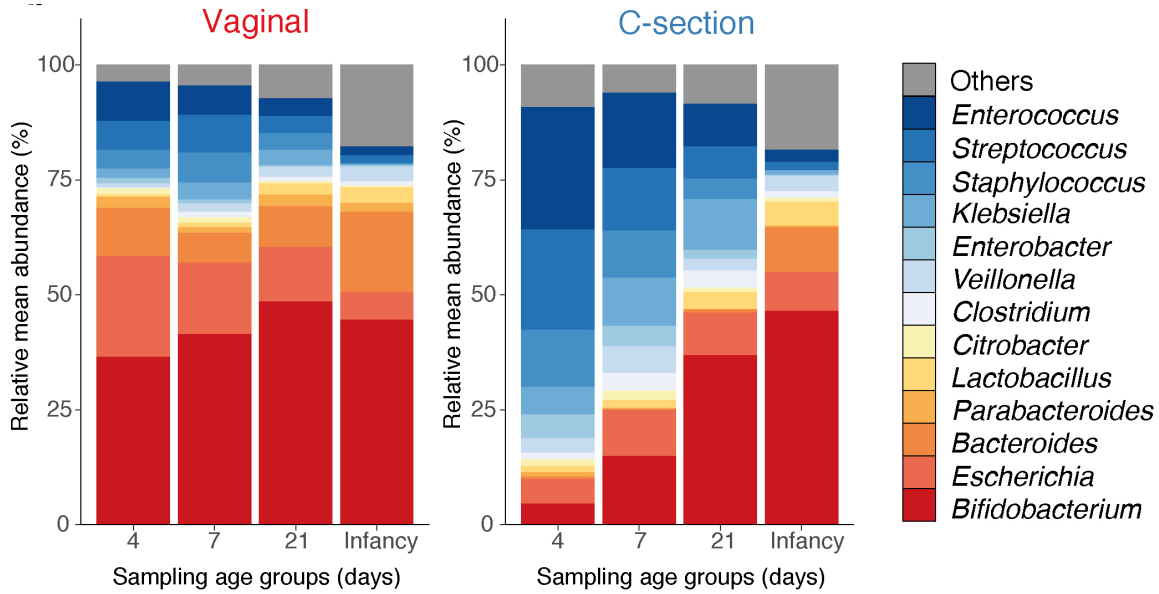

Figure 2.7 Perturbed gut microbiota development associated with caesarean-section birth.

Longitudinal changes in the mean relative abundance of genera of faecal bacteria, sampled on day 4, day 7, day 21 and in infancy, for genera with >1% mean relative abundance across all samples from the neonatal period. Vaginal deliveries, $n = 744$ samples from 310 babies; deliveries via caesarean section, $n = 725$ samples from 281 babies.

2.3.4 Role of breastfeeding in the neonatal period and infancy

Breastfeeding has been known as the most important factor shaping the gut microbiota during infancy (as measured from 3 months of life, Stewart *et al.*, 2018; Vatanen *et al.*, 2018). To determine the role of breastfeeding on the gut microbiota of the BBS babies, I assessed the effect of breastfeeding status (partial and exclusive breastfeeding versus no-breastfeeding, respectively) on the gut microbiota composition through PERMANOVA. To assess if breastfeeding could exert different effects on the gut microbiota of babies born via vaginal or caesarean section, I also analysed the role of breastfeeding stratified by modes of delivery.

In the BBS cohort, breastfeeding status began to exhibit statistically significant effect only from day 7 and exhibited smaller effect (day 7, partial breastfeeding R^2 = 0.742%, p = 0.0043; exclusive breastfeeding R^2 = 1.691%, p = 0.0035; day 21, partial breastfeeding R^2 = 0.777%, p = 0.0234; exclusive breastfeeding R^2=1.868%, p = 0.0070) than mode of delivery (day 7, R^2 = 3.972%, p = 0.0043; day 21, R^2 = 2.408%, p = 0.0234) during the neonatal period (Figure 2.8a, Figure 2.9a). After progressing from neonatal (from day 4 to day 21) to infancy period (at month 8.75 ± 1.98), the impact of breastfeeding became comparable to the impact of delivery mode of delivery in the infancy period (mode of delivery R^2 = 1.004%, p = 0.0240; ongoing (partial) breastfeeding, R^2 = 0.894%, p = 0.0390, Figure 2.4, Table 2.2).

Whilst this finding does not directly validate the central claim of breastfeeding status as the predominant factor of the gut microbiota from months 3 to 14 of life observed in the TEDDY 16S cohort (Stewart *et al.*, 2018), the infancy period R^2 values in this study (up to 2.338% in vaginal-born babies) are comparable to the TEDDY metagenomics cohort (Vatanen *et al.*, 2018) that used the same method (PERMANOVA) to calculate effect size (months 3-6, R^2 = 1.69%, p = 0.0015; months 7-10, R^2 = 1.84%, p = 0.0015), in comparison to the TEDDY 16S cohort which determined R^2 = ~10% based on a different method *EnvFit.*

In addition to differences that might originate from using different statistical analysis methods, the prevalence of breastfeeding also differs between two studies. Over 80% of the BBS babies were exposed to breastfeeding during the neonatal period and remained at this high proportion (86.64%) in the infancy period (8.75 ± 1.98 months, Figure 2.1d, Table 2.1), in contrast to 53% of the TEDDY babies during the same period (months 7-10). The UK-born BBS babies seemed to enter the weaning phase much later than the published large cohorts that highlighted the importance of breastfeeding cessation on microbiota maturation. Only 13.36% of the BBS babies were no longer breastfed by the point of infancy sampling (8.75 ± 1.98 months in the BBS), in contrast to 46% of the TEDDY babies (27% in months 3-6, 72% in months 11-14) and 86% in the Swedish cohort (12-month-old infant, Bäckhed *et al.*, 2015). To fully assess the effect of breastfeeding during later developmental stages in the BBS cohort, future continuous longitudinal samplings of the infancy gut microbiota and detailed dietary information (including the proportional and quantitative weighting of breast milk intake) are warranted.

Furthermore, I did not observe substantially greater effect from breastfeeding after stratification by vaginal and caesarean section babies separately. The effect sizes of breastfeeding (exclusive and partial) were comparable in vaginal and caesarean section babies during the neonatal period (Figure 2.8b-c, Figure 2.9b-c, Table 2.2), suggesting that breastfeeding did not impact the gut microbiota differently according to modes of delivery, during the first few weeks after birth. Interestingly, as the baby progressed from neonatal to infancy period, breastfeeding status began to exhibit greater effect which was only detected in vaginally born babies (R^2 = 1.45% on day 21, R^2 = 2.34% in infancy, Table 2.4), with no significant effect observed in caesarean-section-born babies in these late sampling time points (Figure 2.8b-c, Figure 2.9b-c, Table 2.3). Among vaginally delivered babies, those who stopped breastfeeding at the time of infancy sampling carried significantly lower abundance of breast milk-associated (Soto *et al.*, 2014; Murphy *et al.*, 2017) *Bifidobacterium* and

Lactobacillus (Figure 2.10), relative abundance 48.7% vs 26.0%, p = 0.014 and 3.48% vs 0.69%, p = 0.004, respectively), in comparison to those who still received breastfeeding. This result was in line with the association between the increased level of *Bifidobacterium* with breastfeeding as recently observed in the TEDDY cohort (Stewart *et al.*, 2018; Vatanen *et al.,* 2018).

Finally, it is worth noting that multiple Bifidobacterium strains (i.e. *B. longum, B. breve, B. bifidum*) show dominant presence in the BBS babies, which agrees with the claim of their co-existence within an individual infant gut (Asnicar *et al.*, 2017). These *Bifidobacterium* strains are known to vary in their HMO metabolic activities (Thomson *et al.*, 2018), and capable of driving *Bifidobacterium* dominance through cross-feeding HMOs on the breast milk diet (Milani *et al.*, 2015; Turroni *et al.*, 2018; Nishiyama *et al.*, 2018; Motherway *et al.*, 2018; Lawson *et al.*, 2019), while the other main HMO utiliser *Bacteroides* could compete with the HMO-utilising *Bifidobacterium* strains (e.g. *B. longum*, *B. infantis*), and compensate in the presence of the non-HMO-utilising *Bifidobacterium* strains (e.g. *B. bifidum*, Marcobal *et al.*, 2011; Vatanen *et al.*, 2016). Future BBS investigations will further explore the strain and functional variation of *Bifidobacterium* and *Bacteroides* within and between individuals, and to determine how intra- and inter-species cross-feeding interactions contribute to the diversity and dominance of these genera in early-life gut microbiota through breastfeeding.

In summary, the observed effects of breastfeeding in the BBS agreed with previous findings that continuous exposure to breastfeeding during infancy might have a greater lasting effect, in comparison to the immediate impact of a one-time event such as birth. Interestingly, the lasting effect of breastfeeding seemed to be limited to vaginal born babies only. Whilst this observation contradicted recent claims that the perturbed gut microbiotas of caesarean-section-born babies could be rescued by exclusive breastfeeding (Hill *et al.*, 2017; Liu *et al.*, 2019), it could be potentially explained by birth mode-associated differences in breast milk microbiota reported

in other cohorts (Cabrera-Rubio *et al.*, 2012; Toscano *et al.*, 2017; Hermansson *et al.*, 2019), suggesting the possibility of combinatorial perturbation effect aggregated by aberrant breast milk microbiota in caesarean-section birth. Future studies should strongly consider this line of investigation, while accounting for the compositional variation in the under-studied, cohort-specific breast milk microbiota (Moossavi *et al.*, 2019).

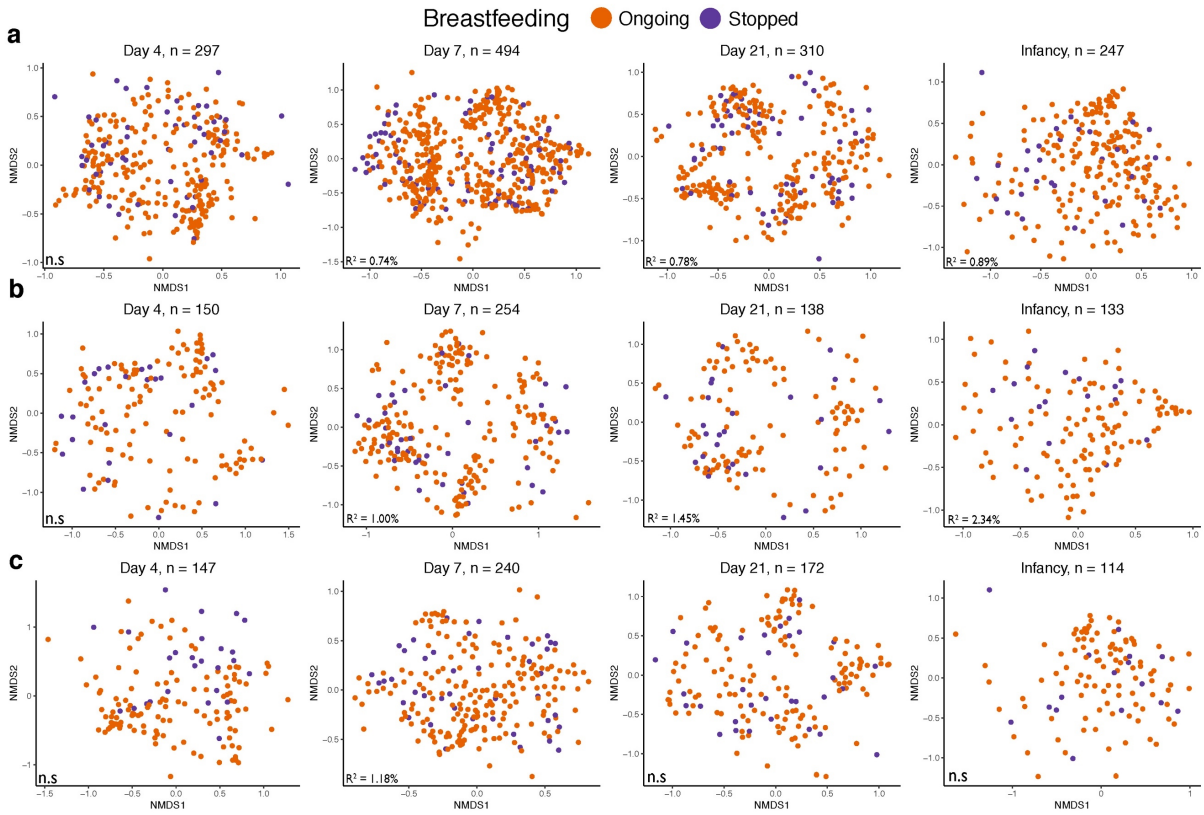

Figure 2.8 Microbiota variation associated with breastfeeding status.

a-c, Non-metric multidimensional scaling (NMDS) ordination of Bray–Curtis dissimilarity between the species relative abundance profiles of the gut microbiota sampled from all BBS babies (**a**), vaginal born babies (**b**) and caesarean-section-born babies (**c**) across four sampling age groups. Microbial variation explained by the breastfeeding status (ongoing versus stopped) in each cross-section test is shown in the bottom left. The ongoing status is defined as if the participant was subjected to either partial or exclusive breastfeeding, whereas the stopped status was classified as no breasting at the time of sampling. All statistical tests were significant (q-value<0.05) unless otherwise stated as "n.s" with PERMANOVA R^2 and p-values reported in Tables 2.2-2.4). Number of breastfed babies on day 4 (total, $n = 245$; vaginal, $n = 124$; caesarean section, $n = 121$), day 7 (total, $n = 411$; vaginal, $n = 213$; caesarean section, $n = 198$), day 21 (total, $n = 251$; vaginal, $n = 111$; caesarean section, $n = 140$), during infancy period (total, $n = 214$; vaginal, n = 116; caesarean section, $n = 98$). Number of non-breastfed babies on day 4 (total, $n = 52$; vaginal, $n = 26$; caesarean section, $n = 26$), day 7 (total, $n = 83$; vaginal, $n = 41$; caesarean section, $n = 42$), day 21 (total, $n = 59$; vaginal, $n = 27$; caesarean section, $n = 32$), during infancy period (total, $n = 33$; vaginal, $n = 17$; caesarean section, $n = 16$).

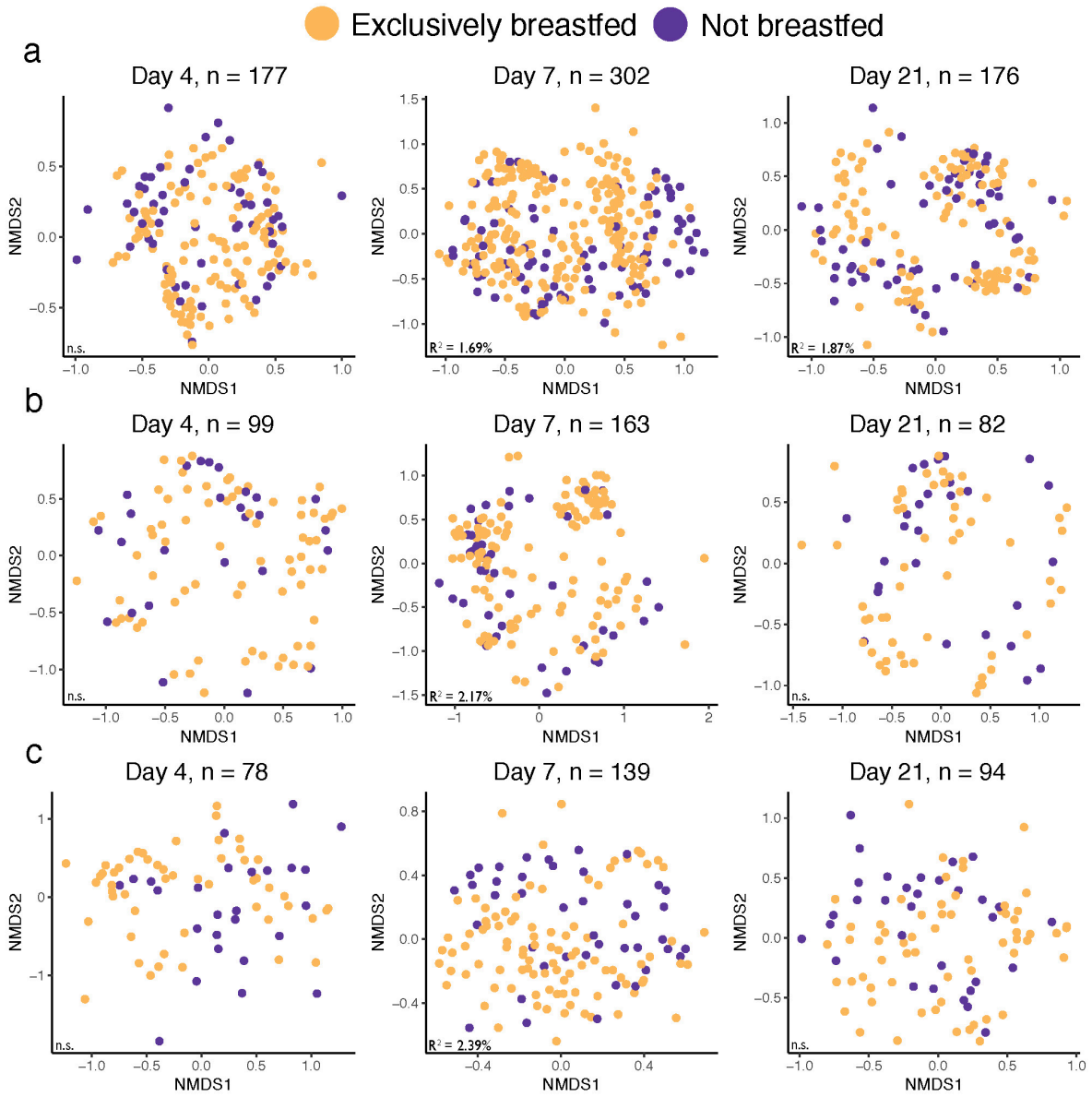

Figure 2.9 Microbiota variation associated with exclusive breastfeeding status.

a-c, Non-metric multidimensional scaling (NMDS) ordination of Bray–Curtis dissimilarity between the species relative abundance profiles of the gut microbiota sampled from all BBS babies (**a**), vaginal born babies (**b**) and caesarean-section-born babies (**c**) across four sampling age groups. Microbial variation explained by the exclusive breastfeeding or non-breastfeeding in each cross-section test is shown in the bottom left. All statistical tests were significant (q-value < 0.05) unless otherwise stated as "n.s" with PERMANOVA R^2 and p-values reported in Tables 2.2-2.4). Number of breastfed babies on day 4 (total, $n = 125$; vaginal, $n = 73$; caesarean section, $n = 52$), day 7 (total, $n = 219$; vaginal, $n = 122$; caesarean section, $n = 97$), day 21 (total, $n = 117$; vaginal, $n = 55$; caesarean section, $n = 62$). Number of non-breastfed babies on day 4 (total, $n = 52$; vaginal, $n = 26$; caesarean section, $n = 26$), day 7 (total, $n = 83$; vaginal, $n = 41$; caesarean section, $n = 42$), day 21 (total, $n = 59$; vaginal, $n = 27$; caesarean section, $n = 32$). Statistical analysis for infancy samples was not performed as only one baby was exclusively breastfed at the point of infancy sampling.

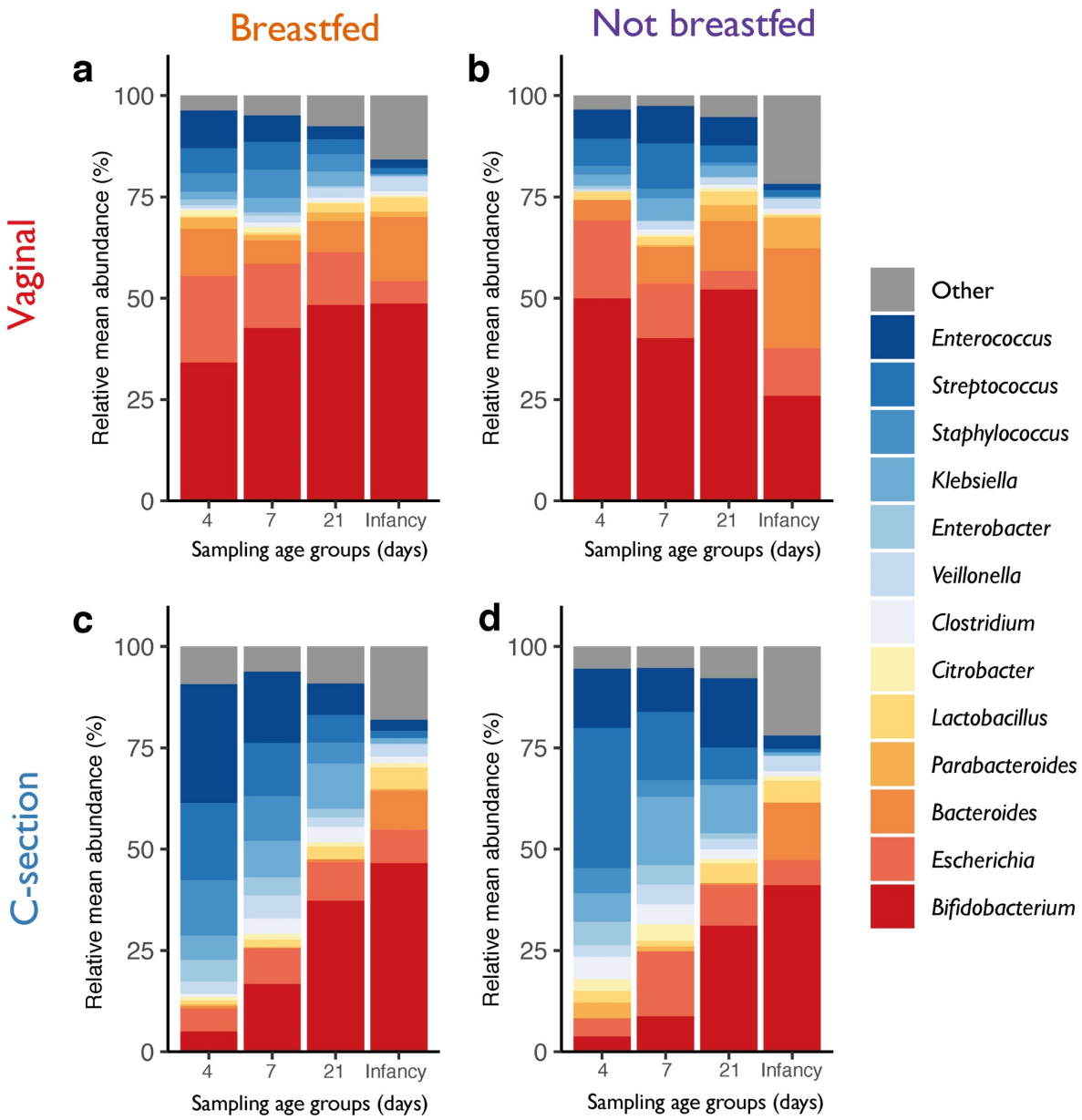

Figure 2.10 Non-breastfeeding associated with depleted *Bifidobacterium* in vaginal born babies in infancy.

a-d, Longitudinal changes in the mean relative abundance (RA) of faecal bacteria at the genus level sampled on day 4, 7, 21 days of life and in infancy, stratified by modes of delivery. Vaginal born babies **(a)** with ongoing breastfeeding at the time of sampling carried significantly higher level of *Parabacteroides* on day 4 (mean relative abundance 2.83% vs. 0.07%, p = 0.042), *Staphylococcus epidermis* on day 7 (mean relative abundance 5.31% vs. 0.94%, p = 0.0007), and *Bifidobacterium* and *Lactobacillus* in infancy (relative abundance 48.7% vs. 26.0%, p = 0.014 and 3.48% vs. 0.69%, p = 0.004, receptively), in comparison to the non-breastfed vaginal babies **(b)**. Caesarean-section-born babies with ongoing breastfeeding **(c)** at the time of sampling carried significantly higher level of *Staphylococcus epidermis* on day 7 and 21 (mean relative abundance 7.62% vs. 1.75% p = 0.043; 3.91% vs. 0.93%, p = 0.030, respectively), in comparison to the non-breastfed, caesarean section (caesarean section) babies **(d)**. Only the genera with > 1% RA across all neonatal period samples are shown. The exact number of subjects in each tested group are listed in the caption of Figure 2.8.

2.3.5 Reduced level of *Bacteroides* associated with perturbations at birth

At birth, newborns delivered vaginally are immediately exposed to the lactobacillus-enriched vaginal communities (Dominguez-Bello *et al.*, 2010). Pioneering work by Dominguez-Bello *et al*. suggested that- compared to babies delivered by caesarean section- the gut microbiota of vaginally delivered babies were enriched in lactobacilli associated with the microbiota of the mother's vagina (Dominguez-Bello *et al.*, 2010; 2016). However, I found a low abundance and prevalence of *Lactobacillus* spp. in the neonatal gut microbiotas. I detected no statistical differences in the prevalence (present at over 1% abundance in 11.9% and 15.7% of the microbiota of babies delivered vaginally or by caesarean section, respectively) or abundance of *Lactobacillus* between babies delivered vaginally (1.217%; 95% confidence interval, 0.81–1.621%) or by caesarean section (2.21%; 95% confidence interval, 1.54–2.88%). While a transient bloom of *Lactobacillus* immediately after birth outside the sampling window of the present study could not be excluded, my observations suggest that vaginal microbiota-associated *Lactobacillus* species were neither common, dominant colonisers of the neonatal gut microbiota nor associated with vaginal birth. The lack of replication of the association between *Lactobacillus* colonisation and vaginal birth, presented here and in all other cohorts, casts strong doubts on the scientific rationale behind "vaginal seeding", a controversial clinical practice that exposes caesarean-section-delivered babies with maternal vaginal fluid in order to "restore" their gut microbiotas (Cunnington *et al.*, 2016; Dominguez-Bello *et al.*, 2016).

Instead, commensal species from the *Bacteroides* genus were detected at high abundance in the gut microbiota of 51.0% (160 out of 314) of vaginally delivered babies (mean relative abundance 8.13%; 95% confidence interval, 6.88–9.39%, Figure 2.11). By contrast, *Bacteroides* species were low or absent in the gut microbiota of 99.6% (281 out of 282) babies delivered by caesarean section (mean relative abundance 0.43%; 95% confidence interval, 0.11–0.74%). In 60.6% (86 out of 142) of the babies delivered by caesarean section, this low-*Bacteroides* profile (see 'Classification of babies with the low-Bacteroides profile' in Methods

for definition of this profile) persisted into infancy, by which point only species of *Bacteroides* were differentially abundant between the gut microbiota of babies delivered vaginally or by caesarean section (Figure 2.5, Figure 2.6, Table 2.5).

It is worth highlighting that nearly half (49.0%, $n = 154$) of the vaginally delivered BBS babies exhibited a low-*Bacteroides* profile, a proportion substantially higher than the 20% previously reported in a Finnish infant cohort ($n = 39$, up to 3 years of age, Yassour *et al.*, 2016). Although it would not be possible to assess the independent effect of maternal exposure to antibiotics during delivery by caesarean section (as antibiotics were administered in all deliveries by caesarean section), among vaginally delivered babies I observed a significant association between the low-*Bacteroides* profile and maternal IAP (odds ratio 1.77, 95% confidence interval, 1.17–2.71%, $P = 0.0074$), which also accounted for the greatest amount of variation in the gut microbiota of vaginally delivered babies ($R^2 = 5.88–13.6\%$, Table 2.4). These results expand on previous findings (Jakobsson *et al.*, 2014; Yassour *et al.*, 2016), and highlight the low-*Bacteroides* profile as a perturbation signature that is associated with delivery by caesarean section (Bäckhed et al., 2015; Bokulich *et al.*, 2016), and with maternal IAP in vaginal delivery (Nogacka *et al.*, 2017; Tapiainen *et al.*, 2019; Azad *et al.*, 2016).

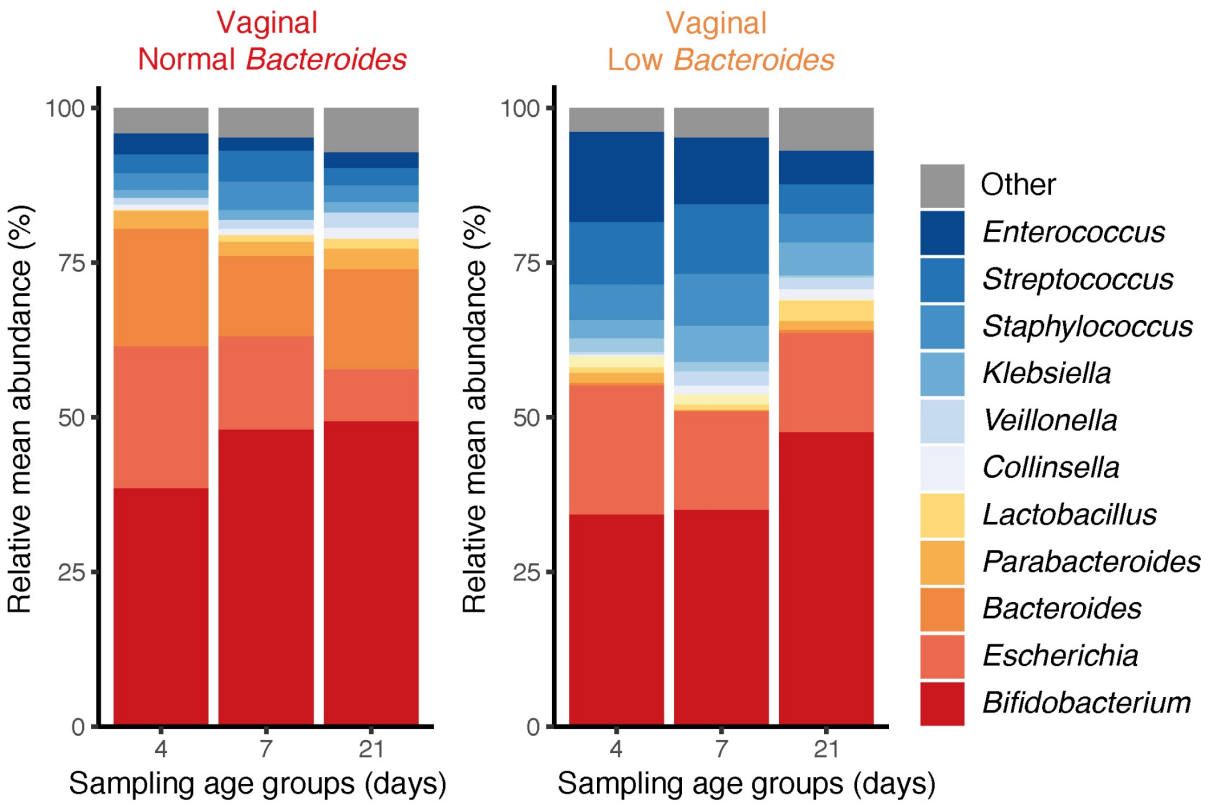

Figure 2.11 Microbial succession in the neonatal gut microbiota of vaginally delivered babies.

Bar plots show longitudinal changes in the mean relative abundance of faecal bacteria at the genus level on day 4, day 7 and day 21, for genera with >1% mean relative abundance across all neonatal samples. Left, $n = 316$ samples from 160 vaginally delivered babies detected with *Bacteroides*. Right, $n = 290$ samples from 154 vaginally delivered babies with the low-*Bacteroides* profile (defined in 'Classification of babies with the low-*Bacteroides* profile' in Methods).

2.3.6 Disrupted transmission of maternal bacterial strains in caesarean-section birth.

The transmission of gastrointestinal bacteria from mothers to their babies is an underappreciated form of maternal kinship (Funkhouser, Bordenstein, 2013). To assess if variation in neonatal microbiota could be attributed to differential transmission of maternal microbiota, I reconstructed the strain-level bacterial transmission events across 178 mother–baby dyads (112 vaginally delivered babies, 66 babies delivered by caesarean section).

Applying rare SNPs as highly sensitive and specific strain markers (Truong *et al.*, 2017), I showed that the majority of transmissions of maternal microbial strains during the neonatal period occurred in vaginally delivered babies (74.39%), at much higher frequency than was observed for babies delivered by caesarean section (12.56%, Fisher's exact test, $P < 0.0001$, Figure 2.12). *Bacteroides* spp., *Parabacteroides* spp., *E. coli* and *Bifidobacterium* spp. were most frequently transmitted from mothers to babies through vaginal birth, consistent with previous observations (Wampach *et al.*, 2018; Nayfach *et al.*, 2016; Ferretti *et al.*, 2018; Yassour *et al.*, 2018).

Overall, phylogenetically related species belonging to the classes *Actinobacteria* and *Bacteroidia* shared a similar pattern for the timing of transmissions (Figure 2.13a). For *Bacteroides* and *Parabacteroides* species (class *Bacteroidia)* such as *B. vulgatus* (Figure 2.13b), the lack of transmission continued far beyond the neonatal period in babies delivered by caesarean section (Nayfach *et al.*, 2016): the transmission of *B. vulgatus* was rarely detected later in infancy. This is in contrast to the transmission pattern of other common early colonisers, including *Bifidobacterium* species from the class *Actinobacteria*, such as *B. longum*, Figure 2.13c) and *E. coli*, for which colonisations of maternal strains occurred more frequently later in infancy (Fisher's exact test, $P = 0.0479$ and $P = 0.0226$, respectively). Interestingly, as previously reported (Korpela *et al.*, 2018b), the other frequently transmitted *Actinobacteria* species *Collinsella aerofaciens* exhibited a highly selective, early transmission pattern as observed in *Bacteroides* species. Taken together, these results highlight the neonatal period as

a critical early window of maternal transmission, as shown by the disrupted transmission of pioneering *Bacteroides* species that is evident in babies delivered by caesarean section (who show long-term absences of these *Bacteroides* species).

This analysis also revealed at least four different modes and strategies of commensal gut microbiota transmission in early life. The transmission of *Bacteroides* species, the most common bacteria in the adult gut microbiota seemed to be primed to occur at the time of birth via the faecal-oral route, a form of physical contact that is unlikely to reoccur later in life; whereas the transmissions of *Bifidobacterium* and *E. coli* strains occurred continuously throughout the neonatal and infancy period, and had multiple sources of transmission not limited to the maternal gut microbiota (e.g. *Bifidobacterium* sp. in breastfeeding), as shown by a large number of detected non-maternal, late transmission strains in infancy samples. Although the spore-forming *Clostridia* (*Blautia wexlerae*, *Ruminococcus torques* in Figure 2.13a) are highly prevalent bacteria found in healthy adults and are known for their ability to spread between people via environmental reservoirs (Browne *et al.*, 2016; 2017), transmission of spore-formers rarely occurred during gut microbiota assembly in very early life, as observed here and in other cohorts (Nayfach *et al.*, 2016; Korpela *et al.*, 2018b). Given the coverage-dependent nature of current metagenomic strain transmission analyses, it is also possible that the endospores were transmitted to newborn babies, but could not germinate to colonise and establish a niche (to be detected) in the neonatal gut microbiota due to colonisation resistance or the absence of germination signal (e.g. bile acids). Lastly, for non-enteric bacteria such as *Streptococcus* species that frequently colonised the neonatal gut microbiota, it is plausible to speculate that they are preferentially acquired from the environment and other body sites (e.g. oral and skin where *Streptococcus* is dominant, Dewhirst *et al.*, 2010; Cogen *et al.*, 2008), rather than the faecal strains from mothers indicating preferred non-faecal transmission routes.

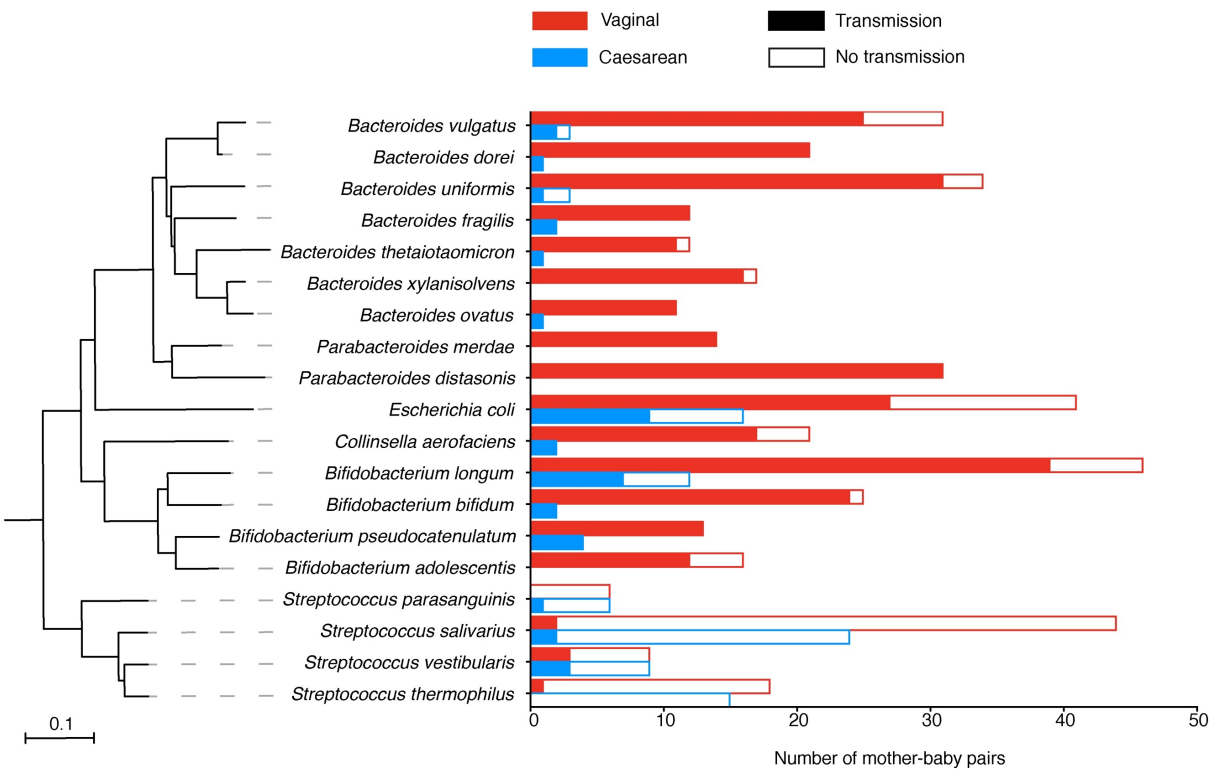

Figure 2.12 Transmission of maternal microbial strains during the early neonatal period.

Transmissions of maternal microbial strains across 178 mother–baby pairs (for 112 vaginally delivered babies, and 66 babies delivered by caesarean section) who sampled at least once during the early neonatal period. Only the frequently shared species that were detected with sufficient coverage for strain analysis in more than ten pairs are shown. The neighbour-joining tree is constructed on the basis of the pairwise mash distances of the respective reference genomes. Phylogenetically related species shared a similar pattern for the timing of transmissions; for example, the frequent transmission of *Bacteroides* spp., *Parabacteroides* spp. and *Bifidobacterium* spp. in vaginally delivered babies and the lack of species of these genera in babies delivered by caesarean section, and the fact that most *Streptococcus* species were transmitted from sources other than the maternal gut microbiota. A summary of early strain transmission events detected in 178 mother-baby pairs presented in this figure is attached as Appendix 3.

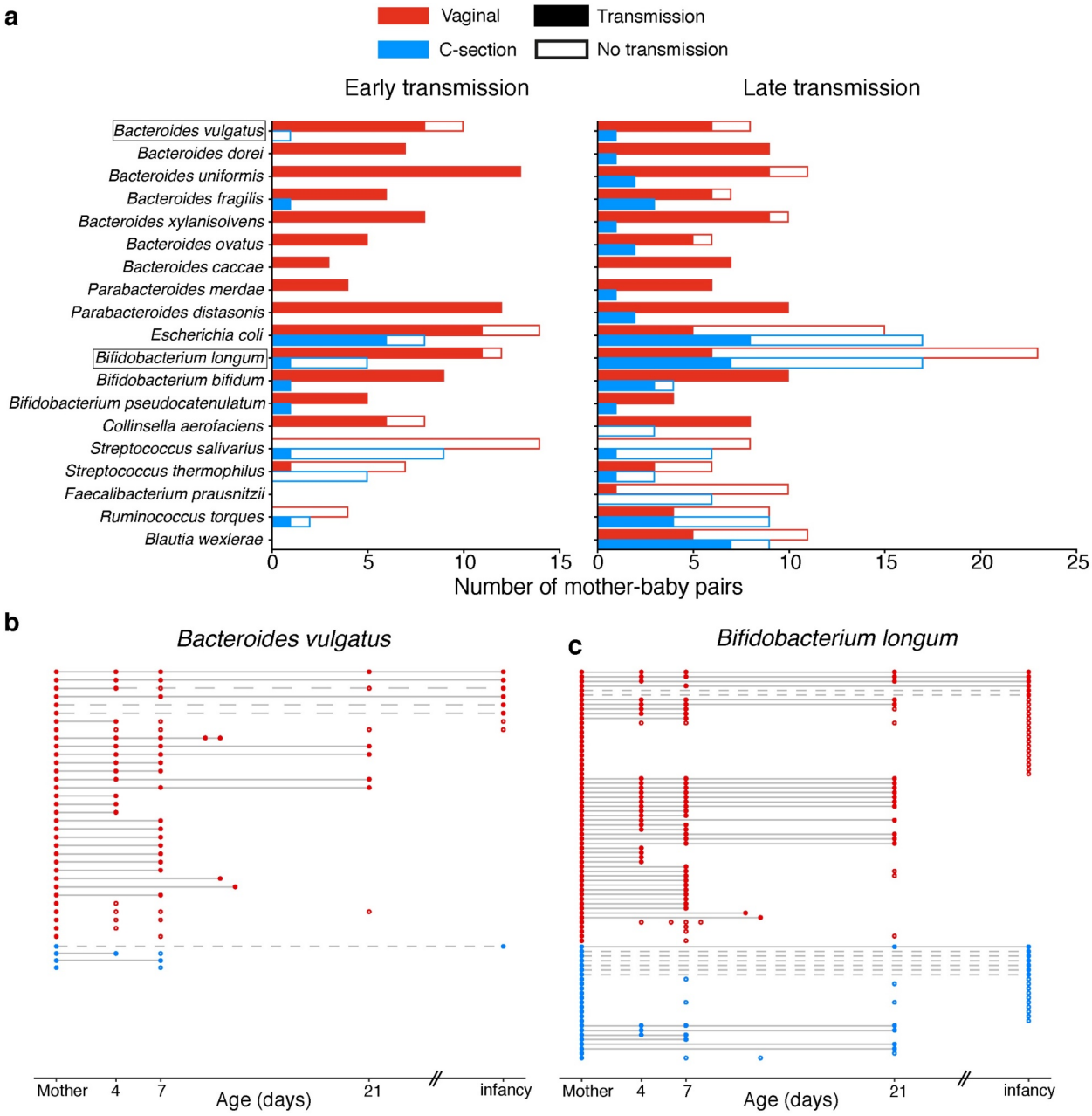

Figure 2.13 Disrupted transmission of maternal microbial strains in caesarean-section births.

a, Early and late transmission of the maternal microbial strains in mother–baby pairs (35 pairs for vaginally delivered babies and 24 pairs for babies delivered by caesarean section), longitudinally sampled during the neonatal (early) and infancy (late) period. Only the frequently shared species that were detected with sufficient coverage for strain analysis in more than ten pairs are shown. **b**, **c**, Transmission events of maternal strains of *B. vulgatus* (**b**) and *B. longum* (**c**) in vaginally delivered babies and babies delivered via caesarean section, over time. In each row of mother–baby paired samples, each circle represents a detectable strain either identical to (filled) or distinct from (hollow) the maternal strain. Across the rows, identical strains are either linked by a solid line (which represents early transmission and persistence to infancy) or a dashed line (which indicates late transmission). A summary of early and late strain transmission events detected in 59 mother-baby pairs presented in this figure is attached as Appendix 4.

2.3.7 Microbiota measurements are robust to sequencing depth variation

Given the measurements of microbiota species and strain presented above are both dependent on sufficient read coverage, I also assessed if sequencing depth variation had any effect on the observed, between-group species and strain-level differences.

On average, 22.4 (95% CI 22.1-22.6) million raw reads were generated per sample. 19.3 (95% CI 19.1-19.6) million reads (87.3% of the raw reads) per sample passed decontamination and quality trimming steps for downstream analysis. I did not observe any statistical difference in the sequencing depth (before or after the quality and contaminant trimming) between vaginal and caesarean-section samples across all sampling age groups except on day 4 (Figure 2.14a-b). Where microbiota species richness measurements were directly relevant in mother-baby species and strain sharing analysis, I found that observed species richness differences between vaginal and caesarean-section-born babies were not affected by sequencing depth variation. For the day 4 gut metagenomes, I observed no correlation between the sequencing depth and species richness; the Spearman correlation coefficient between sequencing depth and Shannon diversity index was -0.002028 (P=0.9716), and -0.06792 (P=0.2331) with the species count (above 0.01% relative abundance used in species sharing measurement). Despite having slightly lower sequencing depth on day 4, the vaginal-born neonatal gut microbiotas still exhibited higher species richness on day 4, as measured by both the species count and alpha (Shannon) diversity (Figure 2.14c-d). I further performed ANOVA tests to confirm that sequencing depth (post trimming) did not interact with the delivery mode in explaining the variance of alpha diversity ($P = 0.59308$) nor species count ($P = 0.9872$) of day 4 gut metagenomes. These data suggest that the species richness measurements of this study are robust to sequencing depth variation, which was only observed in day 4 samples, and did not impact on the observed microbiota species and strain differences between vaginal and caesarean-section-born babies.

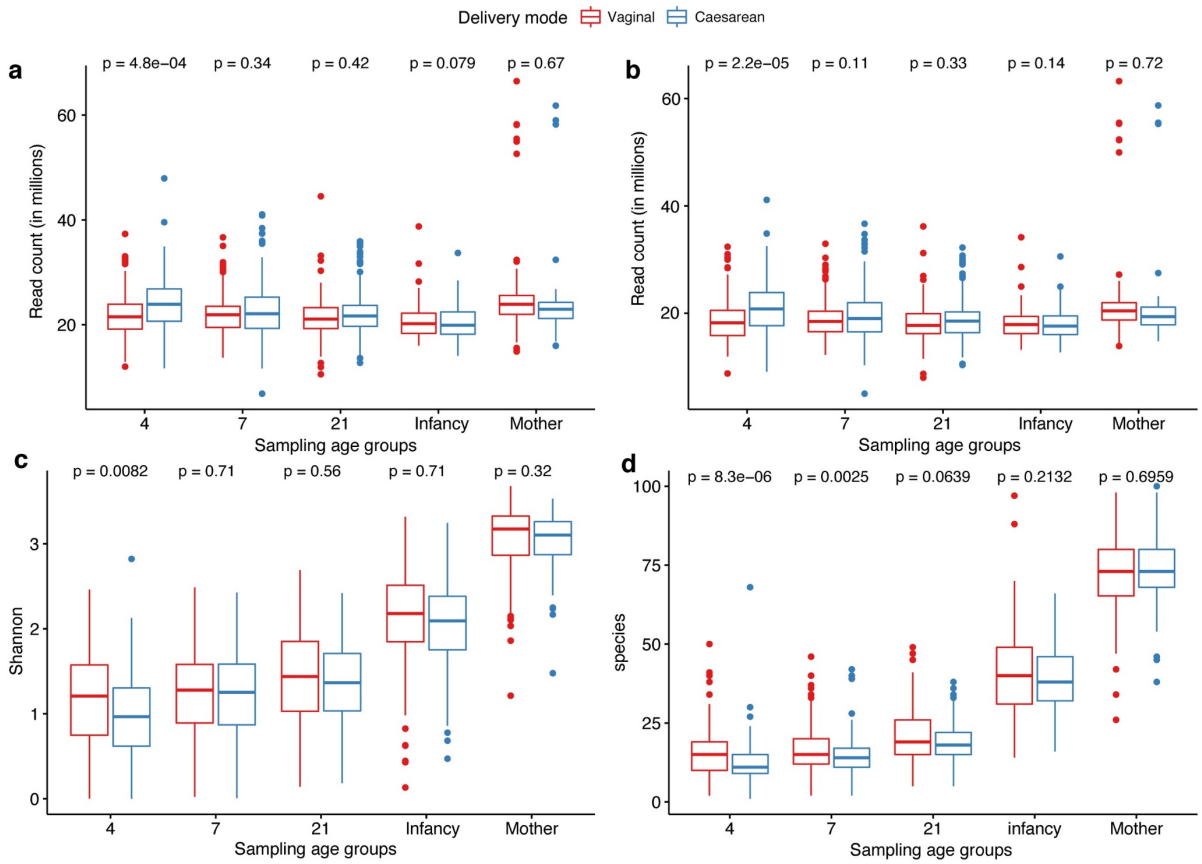

Figure 2.14 Species count and richness are robust to sequencing depth variation.

a-d, Box-plots showing sequencing depth and the measurements of microbiota species richness across five sampling age groups. **a-b**, Number of reads before (**a**) and after quality trimming and decontamination (**b**); **c-d,** Gut microbiota species richness as measured by alpha (Shannon) diversity (**c**) and the number of species present at over 0.01% relative abundance (**d**) per sample. Sequencing depth did not interact with the delivery mode in explaining the variance of alpha diversity (ANOVA, P = 0.59308) nor species count (ANOVA, P = 0.9872) of day 4 gut microbiotas. Significance between groups (modes of delivery) was determined by two-sided Wilcoxon rank-sum test.

2.3.8 Assessment of the impact of short-term storage on the faecal microbiota

In order to assess the feasibility of multi-centre faecal sample collection, as part of the pilot study protocol design, I performed benchmarking experiments to assess whether faecal samples can be sent by post without significant loss of sensitivity in microbiota analysis. I sought to determine the impact of short-term storage on the faecal microbiota diversity and composition by varying the time between sample collection and sample initial processing (DNA extraction), and by varying the storage temperature prior to extraction (room temperature vs 4°C).

In this pilot study, six participants (mothers, n=3; babies, n=3) were recruited with informed written consent at the University College London Hospital maternity unit between February and July 2014. The stool samples were collected at the hospital and then divided into aliquots. DNA was extracted from one aliquot (fresh sample) immediately, and the other samples were stored at ambient temperature and 4°C prior to DNA extraction for 2, 4 and 7 days, respectively. Please refer to the main study SOP for detailed sampling and processing protocols (Bailey *et al.*, 2017) . 16S rRNA sequencing (MiSeq) was used to assess the bacterial population composition of the faecal samples. The V1-V2 hypervariable region of the bacterial 16S rRNA gene was amplified from faecal DNA extracts using the barcoded fusion primers: MiSeq-27F and MiSeq-338R. Illumina-based partial 16S rRNA sequences were processed and sequenced using mothur v1.34.1 and the MiSeq SOP (http://www.mothur.org/wiki/MiSeq_SOP). Low-quality sequences with less than 500 bp sequence length and sequences that had homopolymers longer than 7 bases were removed. Chimeric sequences were removed in mothur using Perseus algorithm. The operational taxonomic unit (OTU) clusters were defined based on the 97% sequence identity cut-off. Results of mothur sequencing analysis were analysed in R v3.2.1 and statistical tests performed in GraphPad Prism v6.

In order to examine the potential loss in species richness and diversity during storage, I stratified by sample storage time and performed a pairwise comparison of alpha diversities between

freshly processed faecal samples with those stored at ambient temperature and 4°C, respectively. I observed no statistical difference in Shannon indexes of the faecal samples stored at ambient temperature and 4°C for 2 or 4 days, in comparison to the same fresh samples processed immediately (paired Wilcoxon tests for 2-day storage at ambient temperature versus fresh, $p = 0.0840$; at 4°C versus fresh, $p = 0.2324$; 4-day storage at ambient temperature versus fresh, $p = 0.1309$, at 4°C versus fresh, $p = 0.3750$). Storing at ambient temperature for 7 days did result in a statistically significant decrease in alpha diversity, but not for 7-day storage at 4°C (paired Wilcoxon tests for ambient temperature versus fresh, $p = 0.0059$; at 4°C versus fresh, $p = 0.0840$). These data suggest that the faecal microbiota richness would not be significantly affected by short term transport/storage for 2-4 days at ambient temperature or at 4°C for up to 7 days.

To establish whether the composition of maternal faeces was affected by storage temperature prior to DNA extraction, I compared the taxonomic relative abundances at the genus level for freshly processed samples and those split and stored at either 4°C or ambient temperature for up to 7 days. I observed no significant difference in the relative abundances of the 20 most prevalent genera (prevalence >50% across all samples, including *Bacteroides*) between different storage temperatures for samples stored for either 2, 4 or 7 days, in comparison to freshly processed samples (Wilcoxon matched-pairs signed-rank tests, $p < 0.05$).

2.4 Conclusions

In this chapter, I undertook the largest, longitudinal metagenomic characterisation of the human gut microbiota in a previously under-sampled neonatal period. I showed that the gut microbiotas were extremely unstable and individualised in the neonatal period, providing novel insights into the dynamic assembly process in very early life. The large sample size and well-balanced (with respect to delivery mode) study design provided sufficient statistical power enabled to examine the effect of various early-life events on the neonatal gut microbiota. I demonstrated that mode of delivery was the most significant factor that shaped the gut microbiota in the first few weeks of life, with the diminished effect persisting into infancy. This result, along with an overwhelming number of similar observations in other smaller cohorts (Penders *et al.*, 2006; Azad *et al.*, 2013; Stokholm *et al.*, 2016; Bäckhed et al., 2015; Wampach *et al.*, 2018; Yassour *et al.*, 2016; Bokulich *et al.*, 2016), provides conclusive evidence against the recent claim (Chu *et al.*, 2017) regarding the lack of impact of the mode of delivery on the early-life gut microbiota. The lack of maternal microbiota transmission in caesarean-section born babies, together with the recent studies refuting *in utero* colonisation from the microbiota-free placenta (de Goffau *et al.*, 2019; Theis *et al.*, 2019), strongly support the consensus view that the gut microbiota colonisation process starts during and after birth. If the placenta was indeed a microbial reservoir for colonisation to occur prior to birth, then one would not expect to detect substantial differences in the initial gut microbiota composition as reported herein.

High-resolution metagenomic species and strain analyses demonstrated that the neonatal period is a critical early window of maternal transmission. I highlighted a perturbed gut microbiota profile in babies delivered by caesarean section that was characterised by disrupted maternal transmission, and delayed colonisation of pioneering commensal bacteria such as *Bifidobacterium* and *E. coli* and particularly the *Bacteroides* species with long-term absence lasting into infancy. Importantly, this low-*Bacteroides* perturbation profile was also found in nearly half of the babies born via vaginal delivery, for which I found was associated with

maternal IAP. Given the important immunostimulatory role of *Bacteroides* (through lipopolysaccharide exposure) during this critical window of immune development (Vatanen *et al*., 2016), future studies involving animal models and long-term cohort studies are needed to establish the causal link between the lack of *Bacteroides* and the risk of developing later-life immune-mediated diseases.

It is commonly assumed that passage through the birth canal seeds the neonatal gut microbiota with the *Lactobacillus* spp. dominating mother's vaginal microbiota, whereas those who are delivered via caesarean section are colonised by the maternal skin microbiota (Dominguez-Bello *et al.*, 2010). Given the observed, universally low carriage of *Lactobacillus* across newborn babies, and the abundant presence of maternally-transmitted *Bifidobacterium* and *Bacteroides* strains in vaginally delivered neonates, this chapter highlights the important role of the mother's gut bacteria, rather than vaginal bacteria in priming the neonatal gut microbiota, casting strong doubts on the rationale of the controversial "vaginal seeding" practice (Cunnington *et al.*, 2016; Dominguez-Bello *et al.*, 2016).

On the other hand, the disrupted and delayed colonisation of maternally-derived commensal bacteria after caesarean-section births seemed to predispose colonisation of bacteria from the local hospital environment, as evident by the dominant carriage of bacteria known as opportunistic pathogens during very early life. In Chapter 3, the high-level presence of opportunistic pathogen species observed in the gut microbiota of caesarean-section-delivered neonates will be examined in greater detail, and further validated through large-scale culturing and whole-genome sequence analysis.

Chapter 3: Opportunistic pathogen colonisation in caesarean-section birth

3.1 Introduction and aims

In Chapter 2, I performed large-scale metagenomic characterisation of the neonatal gut microbiota. I showed that the gut microbiotas of caesarean-section-born newborn babies were deprived of maternal transmission-associated commensal bacteria, but dominated by environmental-associated bacteria, including *Enterococcus*, *Staphylococcus*, *Streptococcus*, *Klebsiella*, *Enterobacter* and *Clostridium* species. The high-level detection of these bacteria *in silico*, most of which are known opportunistic pathogens, in the newborn baby gut is a potentially strikingly alarming observation that warrants further investigation and validation.

In this chapter, I aim to carry out detailed metagenomic analysis of six opportunistic pathogen species to investigate their colonisation patterns in the BBS babies associated with stunted gut microbiotas, including but not limited to those delivered by caesarean section. To experimentally validate the carriage of opportunistic pathogen species, I will carry out a large-scale culturing experiment to isolate over 1,000 opportunistic pathogen isolates from over two hundred raw faecal samples, followed by whole-genome sequencing of over 800 isolates. This will enable me to perform high-resolution phylogenetic analyses of four major opportunistic pathogen species, and to detect the presence of antimicrobial resistance (AMR) genes and virulence factors for each strain, which would be a highly non-trivial task using metagenomic short reads alone.

The aims of the research presented in this chapter are:

- determine the identity and carriage level of the most prevalent opportunistic pathogens;
- for each opportunistic pathogenic species, identify putative maternal transmission events from both metagenomes and isolate genomes;

- for each opportunistic pathogenic species, characterise the population structure and the carriage of AMR and virulence genes, in the context of the public nosocomial and commensal isolates.

3.2 Materials and methods

3.2.1 Classification of the opportunistic pathogen carriage

Total opportunistic pathogen load is estimated by calculating the combined, median relative abundance of all differentially abundant (by delivery mode) opportunistic pathogen species (*C. perfringens*, *E. cloacae*, *E. faecalis*, *E. faecium*, *K. oxytoca* and *K. pneumoniae*) per individual across their neonatal-period samples, and independently for the infancy-period and maternal samples. To prioritise relatively high-level opportunistic-pathogen carriage that was feasible for downstream strain-cultivation experiments, individuals with a median abundance of over 1% total opportunistic-pathogen load were defined as a positive carriage. Whilst this is a very conservative threshold to define opportunistic pathogen carriage, internal benchmarking experiments confirmed that lower thresholds of 0.01% and 0.1% did not preclude the significant difference in opportunistic pathogen carriage (six individual species and overall load, expect *K. pneumoniae* with 0.01% threshold, data not shown). between vaginal and caesarean-section-born babies in the neonatal period.

3.2.2 Bacterial isolation and whole-genome sequencing

Raw faecal samples from neonates, stored in the biobank laboratory at -80 °C, were requested on the basis of faecal carriage of targeted species over 1% relative abundance in metagenomes. Selected frozen faecal aliquots, where available (>100 ng), were couriered on dry ice to the Wellcome Sanger Institute within 6 hours of shipment from the biobank laboratory. Bacterial isolates were cultured using the following culture media: *E. faecium* ChromoSelect Agar Base (Cat. No. 90919, Sigma-Aldrich) for *Enterococcus* spp., CP ChromoSelect Agar (Cat. No. 12398, Sigma-Aldrich) for *Clostridium* spp., Coliform ChromoSelect Agar (Cat. No. 81938, Sigma-Aldrich) and *Klebsiella* ChromoSelect Selective Agar (Cat. No. 90925, Sigma-Aldrich) for species of *Enterobacteriaceae*. Between two and five colonies per sample were picked for full-length 16S rRNA gene sequencing to confirm species identification, as previously

described (Browne *et al.*, 2016). Bacterial isolates with species identifications that were congruent with metagenomic identification were re-streaked and purified for genomic DNA extraction using DNeasy 96 Blood and Tissue Kit (QIAGEN, Cat. No. 69581).

DNA sequencing was performed on the Illumina HiSeq X, generating paired-end reads (2 × 151 bp) with a minimum of 50× coverage. Multiple strains per species per faecal sample were also sequenced on the basis of variation across the full-length 16S rRNA sequences. Bacterial genomes were assembled using Velvet v1.2.09 (Zerbino and Birney, 2008) and annotated using Prokka v1.13 (Seemann, 2014) , as implemented in the Sanger Institute Pathogen Informatics pipeline (Page *et al.*, 2016). Genome assemblies were subjected to quality-checking and contaminant-screening with CheckM v1.0.12 (Parks *et al.*, 2015) and Mash Screen v2.1 (Ondov *et al.*, 2019), respectively. Where applicable, the suspected contaminant (non-target organism) sequences were confirmed, and filtered out via raw read-mapping using Bowtie2 v.2.3.0 (Ben Langmead, Salzberg, 2012), before re-assembly.

3.2.3 Bacterial phylogenetic analysis

The phylogenetic analysis of the complete diverse species collection was conducted by extracting the amino acid sequences of 40 universal core marker genes (Sorek *et al.*, 2007; Ciccarelli *et al.*, 2006) from the BBS bacterial culture collection using SpecI (Mende *et al.*, 2013). The protein sequences were concatenated and aligned with MAFFT v.7.2040, and maximum-likelihood trees were constructed using RAxML (Stamatakis, 2014) with default settings. The four most-prevalent opportunistic-pathogen species (*E. faecalis*, *E. cloacae*, *K. oxytoca* and *K. pneumoniae*) in the BBS collection were further analysed in the context of the public genomes, including the UK-hospital strain collections (Raven *et al.*, 2016; Moradigaravand *et al.*, 2016; 2017a; 2017b), the gut-microbiota-cultured strains from the Human Gastrointestinal Bacteria Genome Collection (Forster *et al.*, 2019) and the Culturable

Genome Reference (Zou *et al.*, 2019) collections, and the environmental strains on the Genome Taxonomy Database (v.86, Parks *et al.*, 2018).

To generate phylogenetic trees of individual species, the public genome assemblies were combined with the assemblies of the study isolates, annotated with Prokka v1.13 (Seemann, 2014), and a pan-genome was estimated using Roary v1.007001 (Page *et al.*, 2015). In situations where multiple identical strains (no difference in SNPs in the species core genome) were cultured from the same faecal sample, only one representative strain was included in the species phylogenetic trees. A 95% identity cut-off was used, and core genes were defined as those in 99% of isolates (unless stated otherwise), as as implemented by default in Roary. A maximum-likelihood tree of the SNPs in the core genes was created using RAxMLv8.0.0 (Stamatakis, 2014) and 100 bootstraps. To illustrate the population structure of the closely related *Enterobacter* and *Klebsiella* strain isolates, FastANI v1.1 (Jain *et al.*, 2018) was used to estimate the pairwise average nucleotide-identity distance between all public and BBS genome assemblies, which was then used as an input to generate a neighbour-joining with BIONJ (Gascuel, 1997). All phylogenetic trees were visualised in iTOL (Letunic, Bork, 2016). Sequence types were determined using MLSTcheck v2.1.1630910 (Page *et al.*, 2016), which was used to compare the assembled genomes against the MLST database for the four corresponding major species.

3.2.4 Detecting virulence and resistance genes

ABRicate (v.0.8.13, https://github.com/tseemann/abricate) was used to screen for known, acquired resistance genes and virulence factors against bacterial genome assemblies. For genes related to antimicrobial resistance (AMR), a comprehensive BLAST database that integrates 5,556 non-redundant sequences in the NCBI Bacterial Antimicrobial Resistance Reference Gene Database (PRJNA313047), the Comprehensive Antibiotic Resistance Database (v.2.0.3, Jia *et al.*, 2017), ARG-ANNOT (Gupta *et al.*, 2014) and ResFinder (Zankari *et al.*, 2012) was queried. Three thousand two hundred and two non-redundant, experimentally validated core

virulence genes in VFDB (version 5 October 2018, Chen *et al.*, 2005) were included to build a BLAST database for virulence-factor screening with blastn v2.9.0 using ABRicate default settings (75% nucleotide similarity threshold).

3.2.5 Analysis of transmission of maternal opportunistic pathogen strains

The same approach and strain-distance threshold (core-genome single-nucleotide polymorphisms (SNPs)) described in Chapter 2 for strain transmission analysis with metagenomics data, were applied to the cultured strains to count the number of identical and distinct strains within mother–baby and longitudinal paired samples.

3.2.6 Statistical analysis

The univariate statistical tests of between-group comparisons of species-level abundance and frequency of occurrence were performed using two-sided Wilcoxon signed-rank test and Fisher's exact tests, respectively.

For multivariate statistical analysis, MaAsLin (Morgan *et al.*, 2012) was used for the adjustment of covariates when determining the significance of species associated with a specific variable, while accounting for potentially confounding covariates, as previously described (Stewart *et al.*, 2018; Vatanen *et al.,* 2018). All the covariates that were tested in the PERMANOVA were included in the adjustment, along with the sequencing depth used as a fixed effect. The default MaAsLin parameters were applied (maximum percentage of samples with missing metadata of 10%, minimum percentage relative abundance of 0.01%, $P < 0.05$, $q < 0.25$). Results were visualised using *ggplot2* (Wickham, 2016) in RStudio.

To assess whether the trade-off between the observed level of *Bacteroides* and opportunistic pathogens was an artefact of compositional effects, the proportion of abundances and reads that corresponded to *Bacteroides* were removed separately, before relative-abundance normalization. In the normalised datasets, the statistical enrichment of opportunistic pathogen

species in babies delivered via caesarean-section was consistent with the observation with the original data.

3.2.7 Data availability

The sequencing reads and assemblies generated and analysed in this study have been deposited in the European Nucleotide Archive under accession numbers ERP024601. The bacterial isolates are available from the Lawley Lab upon request.

3.3 Results and discussion

3.3.1 Opportunistic pathogen species enrichment in babies born by caesarean section.

To identify the differentially abundant species between the gut microbiotas of the vaginal and caesarean-section-born babies, I performed univariate comparisons of their microbiota species profiles sampled during the first 21 days of life. By considering the mean relative abundance across all neonatal period (day 4 to 21) samples, six species were found to enriched in the gut microbiota of babies delivered by caesarean section, including *E. faecalis*, *E. faecium*, *E. cloacae*, *K. pneumoniae*, *K. oxytoca* and *C. perfringens* (Figure 3.1a), all of which are known as opportunistic pathogens commonly present in the hospital and healthcare environments. Importantly, some of them are also members of the ESKAPE (*E. faecium*, *Staphylococcus aureus*, *K. pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter* spp.) pathogens that are responsible for the majority of nosocomial infections (Boucher *et al.*, 2009).

Among babies delivered by caesarean section, 83.7% carried opportunistic-pathogen species during the neonatal period (as defined in 'Classification of the opportunistic pathogen carriage' in Methods), in comparison to 49.4% of the vaginally delivered babies and 6.85% in adults (Figure 3.1a). During the first 21 days of life, these opportunistic pathogens accounted for 30.4% (95% confidence interval, 27.86–32.96%) of the species-level abundance in the gut microbiota of babies delivered by caesarean section, compared to 9.8% (95% confidence interval, 8.19–11.4%) in the vaginally delivered babies and 0.55% in adults (95% confidence interval, 0–0.073%). The greatest differences in both the individual and overall opportunistic pathogen carriage were recorded at the earliest sampling point after birth on day 4 of life and remained statistically significant throughout the neonatal period, with the exception of two *Klebsiella* species on day 4 (Figure 3.1b). Longitudinally, the difference in the combined opportunistic pathogen load persisted in the babies delivered by caesarean section who were

resampled later during infancy (abundance in babies delivered by caesarean section of 2.8%, versus 1.6% in vaginally delivered babies; $P = 0.0375$, Welch's t-test).

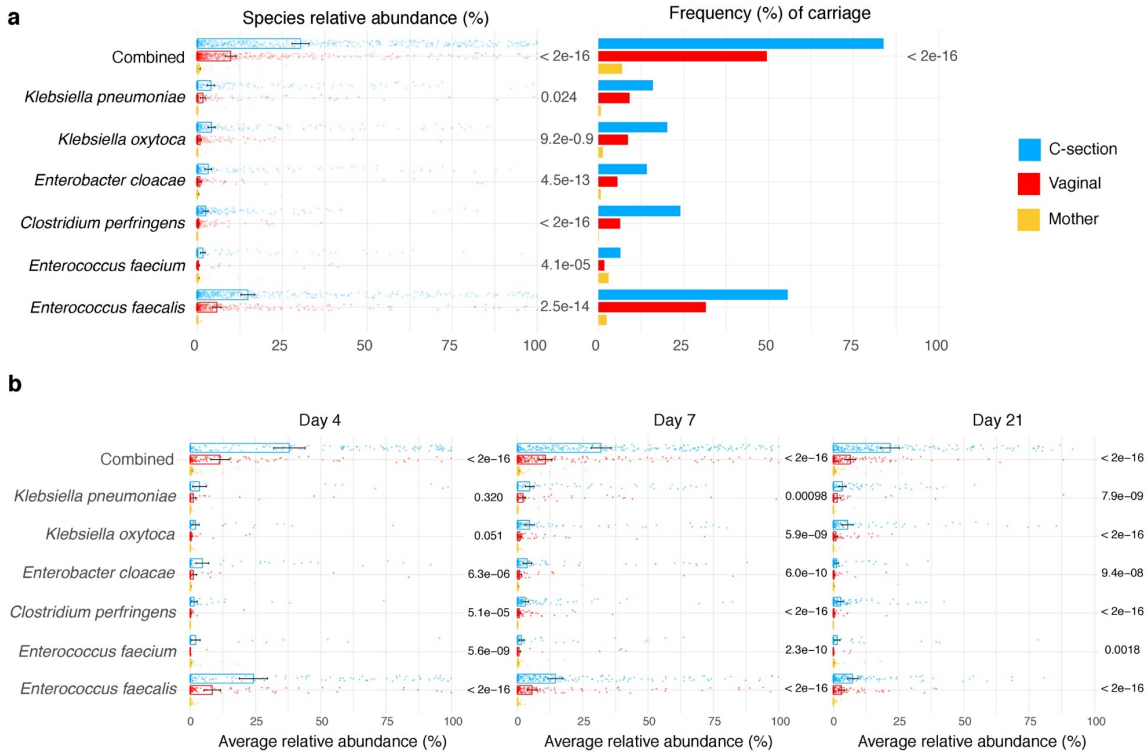

Figure 3.1 Extensive and frequent colonisation of babies delivered by caesarean section with diverse opportunistic pathogens.

a-b, The mean relative abundance and frequency (>1% mean relative abundance) of six opportunistic-pathogen species that are enriched in babies delivered via caesarean section ($n = 596$ samples), compared to vaginally delivered babies ($n = 606$ samples) during the first 21 days of life **(a)**, and at each major neonatal-period sampling group (**b,** day 4 ($n = 310$ individuals, day 7 ($n = 532$ individuals) and day 21 ($n = 325$ individuals)), in the context of the maternal-level carriage ($n = 175$ individuals). Error bars indicate the 95% confidence interval of the mean relative abundance. The significance (P values indicated to the right of the bars) of the difference in mean relative abundance and combined pathogen carriage frequency between babies delivered vaginally or via caesarean section was determined by two-sided Wilcoxon signed-rank test and Fisher's exact tests, respectively.

3.3.2 Opportunistic pathogens in vaginal-born babies with the low-*Bacteroides* profile.

In Chapter 2, I identified a group of vaginally delivered babies who had the low-*Bacteroides* profile, which was associated with maternal IAP. Here, I report that the frequent and abundant carriage of opportunistic pathogens also occurred in this group of babies. During the neonatal period, they were more likely to carry opportunistic pathogens (frequency of carriage 54.5% versus 30.1%, P=0.0023, Fisher's test), and at a higher level than the other vaginal delivered babies (mean relative abundance 30.0% versus 10.2%, P=0.0004, Welch's t-test, Figure 3.2); this pattern also applied to individual opportunistic pathogen species, with the exception of *K. pneumoniae* and *E. faecium*. Overall, the babies who carried opportunistic pathogens during the neonatal period were more likely to have a higher load of opportunistic pathogen carriage when resampled later during infancy (8.75 ± 1.98 months of age, mean relative abundance 2.55% versus 1.48%, P=0.0418, Welch's t-test). These results indicate that the absence of maternal transmission-associated *Bacteroides* colonisation in caesarean-section delivery, and vaginal delivery with maternal IAP seems to have predisposed newborn babies to frequent primary colonisation of opportunistic pathogens.

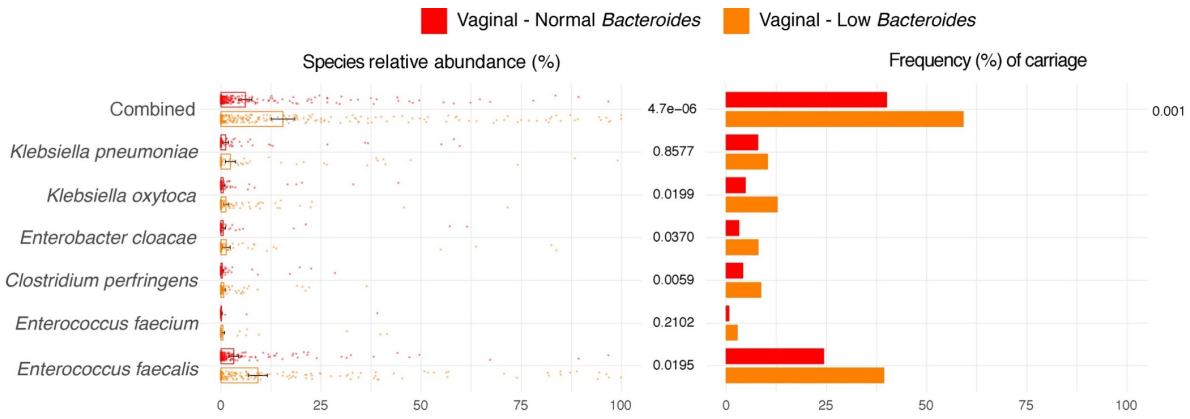

Figure 3.2 Opportunistic pathogen colonisation in vaginally delivered babies with the low-*Bacteroides* profile.

Vaginally delivered babies with the low-*Bacteroides* profile more frequently carried opportunistic pathogens and at higher levels of species relative abundances during the first 21 days of life, as compared to vaginally delivered babies with the normal *Bacteroides* profile. The numbers of individuals sampled in the neonatal period were 160 (vaginally delivered, and with a normal level of *Bacteroides*) and 154 (vaginally delivered, with the low-*Bacteroides* profile). Error bars indicate the 95% confidence interval of the mean relative abundance. Significance in mean species relative abundance and combined pathogen carriage (defined in 'Classification of the opportunistic pathogen carriage' in Methods) frequency was obtained by applying two-sided Wilcoxon signed-rank test and Fisher's exact test, respectively.

3.3.3 Opportunistic pathogen measurement is independent to the level of *Bacteroides.*

Given the prior observation of the depletion of *Bacteroides* associated with caesarean-section birth (Section 2.3.5), and that only relative (rather than absolute) abundance measurements could be reported in this study, the increased relative abundance and prevalence of the opportunistic pathogens reported here could potentially be the effect of the compositionality problem that could lead to the misinterpretation of metagenomics data (Gloor *et al.*, 2017). The observation that samples from vaginally delivered babies with the low-*Bacteroides* profile were also enriched with opportunistic pathogen species would be consistent with this line of inquiry.

To assess if the observed trade-off between taxa were subjected to compositionality effects, one approach is to test if the count measurement of one group is dependent on the other; for instance, a higher load of opportunistic pathogen species would only be found in samples with low *Bacteroides* load, and vice versa. Here, I took this approach and re-analysed the between-group opportunistic pathogens carriage through re-normalisations of the microbiome species profile by separately removing the proportion of relative abundance (Figure 3.3a-b) and raw reads (Figure 3.3c-d) corresponding to *Bacteroides* species. In both cases, the statistical enrichment in the relative abundance and overall frequency carriage of opportunistic pathogen species in caesarean-section-born compared to vaginal-born babies remained significant, and consistent with the primary observation based on the unnormalised data (with *Bacteroides*). This confirmed that the observed between-group differences based on the relative abundances of opportunistic pathogen species were independent to the level of *Bacteroides*. Nevertheless, to definitively address the issue of compositionality, absolute quantitative measurements of bacterial cell counts are needed (Almeida, Shao, 2018). Although the experimental setup of current study did not permit retrospective quantification and comparison of absolute species abundances, novel microbiome-quantification protocols could (Vandeputte *et al.*, 2017; Jian *et al.*, 2018; Morton *et al.*, 2019) facilitate precise measurement of microbial load in faecal

samples (e.g. pathogen species in BBS study), and should be implemented in future large-scale microbiome studies.

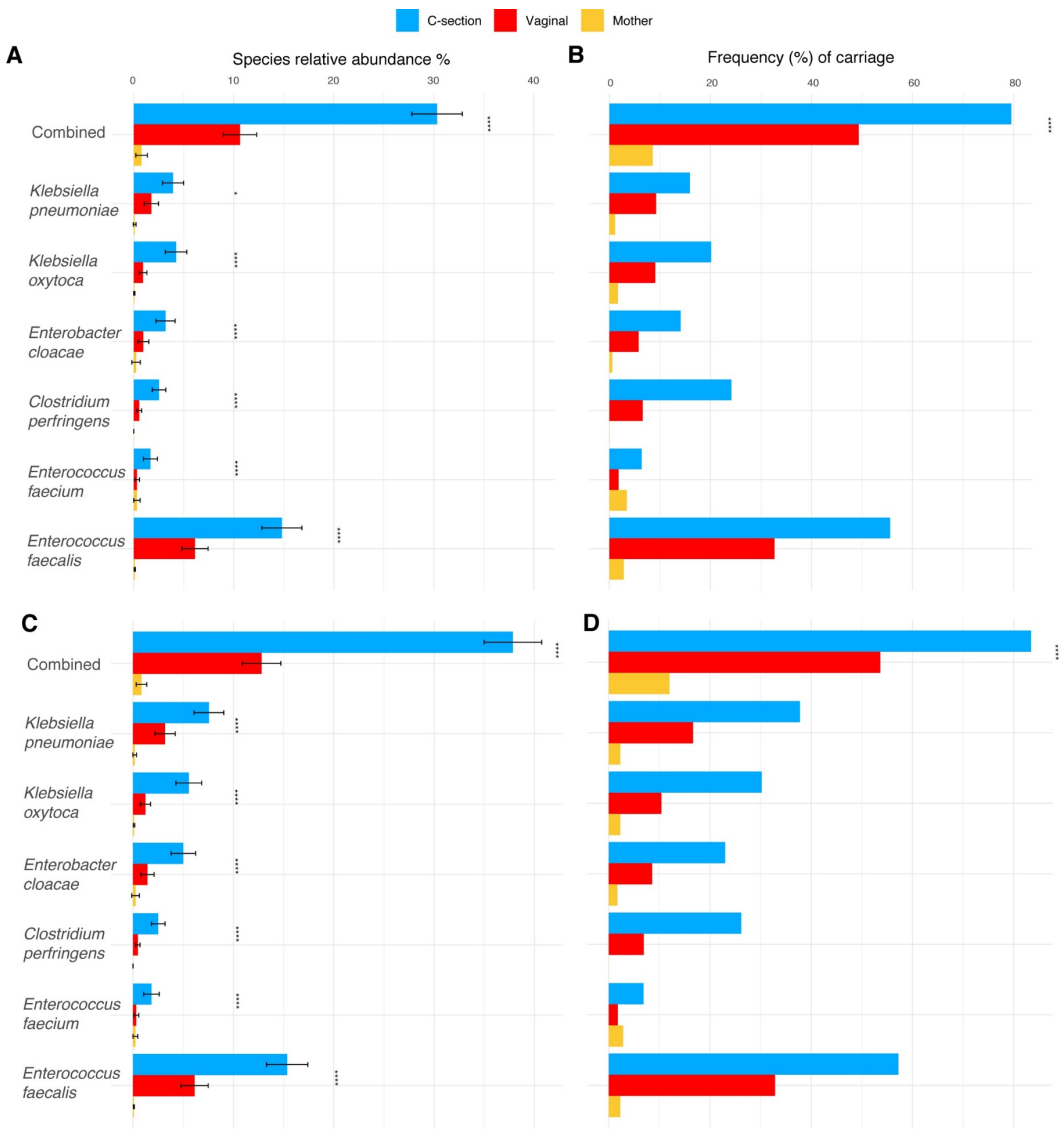

Figure 3.3 The trade-off between the level of *Bacteroides* and opportunistic pathogens is not an artefact of compositionality effects.

Abundance and prevalence of opportunistic pathogen species after re-normalisation by removing the proportion of abundances and reads matching to *Bacteroides.* Abundance (**a, c**) and prevalence (**b, d**) of opportunistic pathogen species during the first 21 days of life, after normalisation by removing relative abundance corresponding to *Bacteroides* (**a-b**), and after normalisation by removing reads assigned to *Bacteroides* (**c-d**). The statistical enrichment of opportunistic pathogen species in caesarean section (C-section) babies was consistent with the original unnormalised metagenomic data. The statistical significance of the difference in mean relative abundance and combined pathogen carriage frequency between babies delivered vaginally (red) and via caesarean section (blue) was determined by two-sided Wilcoxon signed-rank test and Fisher's exact tests, respectively. ****P<0.0001, ***P < 0.001, **P < 0.01, *P < 0.05.

3.3.4 Opportunistic pathogens in non-breastfed babies.

To test the robustness of the significant association between opportunistic pathogen species with modes of delivery, and other clinical covariates that were not considered in the previous univariate analysis, I performed multivariate linear modelling (MaAsLin) analysis.

I stratified the MaAsLin analysis by age groups, and the results confirmed the significant association between opportunistic pathogen species with caesarean-section birth, after adjusting for the potential confounders, including the sequencing depth. All six opportunistic pathogen species identified in the univariate analyses were enriched in caesarean-section-born babies at one or more neonatal period sampling points (Table 3.1).

While the multivariate association analysis supported the main conclusion regarding species association with modes of delivery, it also suggested a link between higher carriage of opportunistic pathogen species with non-breastfeeding status in the neonatal period (day 4: *C. perfringens*, day 7: *K. oxytoca*; day 21: *K. oxytoca* and *E. faecalis*, Table 3.1). This result agreed with recent observations that non-breasting (Pärnänen *et al.*, 2018) and indirect breastfeeding (Moossavi *et al.*, 2019; Cong *et al.*, 2017) during the first 6 months of life was associated with higher abundances of *Streptococcaceae* associated with diarrhoea (Ho *et al.*, 2018), and antimicrobial resistance-enriched *Enterobacteriaceae*, a family that comprised opportunistic pathogens *Klebsiella* and *Enterobacter* species.

Taken together, the consistent reports of increased opportunistic pathogen carriage associated with early non-breastfeeding highlight a potential link for its disease association with necrotising enterocolitis (Lucas, Cole, 1990) and childhood diarrhoea (Subramanian *et al.*, 2014; The *et al.*, 2018). Future studies are warranted to determine if, and how the breastfeeding-associated bacteria provided colonisation resistance to opportunistic pathogen colonisation in very early life.

Age	Variable	Value	Species	Effect size	N	N.not .NA	p-value	q-value
Day 4	Hospital	B	*Enterococcus faecalis*	-0.1535343	310	196	0.01137098	0.1991459
Day 21	Hospital	B	*Klebsiella pneumoniae*	-0.0701723	325	90	0.00202226	0.07610159
Day 4	Delivery_mode	Vaginal	*Enterococcus faecalis*	-0.2118591	310	196	4.85E-05	0.00131014
Day 4	Delivery_mode	Vaginal	*Enterobacter cloacae*	-0.0619815	310	73	0.00431517	0.05377371
Day 4	Delivery_mode	Vaginal	*Clostridium perfringens*	-0.0297215	310	44	0.00619495	0.06921253
Day 7	Delivery_mode	Vaginal	*Enterococcus faecalis*	-0.1675784	532	352	1.57E-12	2.68E-10
Day 7	Delivery_mode	Vaginal	*Klebsiella oxytoca*	-0.0660725	532	130	1.61E-05	0.00032402
Day 7	Delivery_mode	Vaginal	*Enterobacter cloacae*	-0.0568811	532	152	4.57E-05	0.00086902
Day 7	Delivery_mode	Vaginal	*Clostridium perfringens*	-0.0538286	532	159	3.96E-06	0.00010423
Day 7	Delivery_mode	Vaginal	*Klebsiella pneumoniae*	-0.0182554	532	129	0.0102952	0.11002993
Day 21	Delivery_mode	Vaginal	*Enterococcus faecalis*	-0.0700231	325	253	0.00069044	0.01522427
Day 21	Delivery_mode	Vaginal	*Clostridium perfringens*	-0.0532979	325	132	6.84E-11	3.01E-08
Day 21	Delivery_mode	Vaginal	*Enterococcus faecium*	-0.0296704	325	41	0.01523203	0.20991645
Day 21	Delivery_mode	Vaginal	*Klebsiella oxytoca*	-0.0028687	325	157	0.00193736	0.03883527
Day 4	Breastfeeding_status	Yes	*Clostridium perfringens*	-0.0485022	310	44	0.0009727	0.01575775
Day 7	Breastfeeding_status	Yes	*Klebsiella oxytoca*	-0.0480902	532	130	0.0223055	0.21795655
Day 21	Breastfeeding_status	Yes	*Enterococcus faecalis*	-0.0562748	325	253	0.01734168	0.22058155
Day 21	Breastfeeding_status	Yes	*Klebsiella oxytoca*	-0.0034408	325	157	0.00125431	0.02634043
Day 21	Abx_mother_after_hospital	Yes	*Klebsiella pneumoniae*	0.20869748	325	120	2.55E-07	2.81E-05

Table 3.1 Significant opportunistic pathogen species in multivariate statistical analysis.

A list of opportunistic pathogen species associated with clinical covariates ('Variable') in each sampling age group, after accounting for potentially confounding covariate with MaAsLin. Value indicated the direction together with the sign of the effect size; Effect size: the fixed effect coefficient (obtained from the linear model) of the effect for the given outcome; N: number of samples used in this comparison; N > 0: number of non-NA samples used in this comparison; p-value: nominal p-value (two-sided) for the given association; q-value: FDR corrected p-value, q-value, for the given association.

3.3.5 Under-reported opportunistic pathogen carriage in previous studies.

The extensive and frequent opportunistic pathogen colonisations observed in the BBS babies is an unexpected novel finding that had not been previously reported in healthy, full-term delivered newborn babies. Prior to this study, the extensive and frequent colonisation of opportunistic pathogens in the early-life gut microbiota were also reported in term newborns delivered by caesarean section via culturing (Stokholm *et al.*, 2016), and frequently in hospitalised pre-term and low-birthweight newborns who were densely sampled during the very early-life period (Gibson *et al.*, 2016; Raveh-Sadka *et al.*, 2015; 2016; Olm *et al.*, 2017; Rose *et al.*, 2017; Murono *et al.*, 1993). Furthermore, asymptomatic colonisation of hospital-associated *C. difficile* was known to be common among neonates (Rousseau *et al.*, 2012), in particular in those delivered via caesarean section (Penders *et al.*, 2006).

In this section, by re-analysing the publicly available data of other microbiome cohort studies, I show that the caesarean-section-born babies in other cohorts did carry a higher level of opportunistic pathogens, but these were not reported either due to small effect size or inadequate statistical power due to cohorts having much smaller sample sizes of the neonatal period sampling.

Among the few neonatal gut microbiome datasets in public repositories, I focused on two most relevant studies in terms of the sampling period (<30 days of age) and sample size (≥100 cross-sectional samples), namely a Swedish shotgun-based cohort (Bäckhed et al., 2015), and a US 16S rRNA amplicon-sequencing-based cohort (Chu *et al.*, 2017).

In the Swedish cohort, Bäckhed *et al*. presented the data of 95 neonatal (referred to as 'newborn' in the paper) samples from 80 vaginal and 15 caesarean-section babies. Among the species with the greatest difference in relative abundance between vaginal and caesarean-section babies, four of the top five were opportunistic pathogen species, although they were not necessarily supported by statistical significance (Wilcoxon rank-sum test). Some of these opportunistic

pathogens overlapped with the ones identified in this study, included *Enterococcus faecalis* (vaginal 2.64%, caesarean section 7.68%, p = 0.0980), *Enterobacter aerogenes* (vaginal 0.00%, caesarean section 5.25%, p = 0.5362*), Enterobacter hormaechei/Enterobacter cancerogenus* (vaginal 0.01%, caesarean section 12.12%, p = 0.0277) and *Haemophilus parainfluenzae* (vaginal 1.28%, caesarean section 7.95%, p = 1.46E-07). Furthermore, *C. perfringens* was also found to be more abundant in caesarean-section newborns (vaginal 0.55%, caesarean section 1.67%, p = 0.17).

In the 16S rRNA gene-sequenced cohort of 116 neonatal samples (meconium) from 83 vaginal and 33 caesarean section babies, I found that three out of the five most differently abundant genera in caesarean-section (versus vaginal) babies were associated with known opportunistic pathogen species (Chu *et al.*, 2017). These genera included *Neisseria* (incl. *N. meningitidis/gonorrhoeae*; vaginal 0.17%, caesarean section 3.21%, p = 0.0107), *Klebsiella* (vaginal 5.77%, caesarean section 8.01%, p = 0.613) and *Serratia* (incl. *S. marcescens*; vaginal 0.001%, caesarean section 1.16%, p = 0.9075), which could not be identified at the species/strain level due to the detection limit of 16S rRNA gene amplicon sequencing.

Previous cohorts of comparable (or larger) sample sizes such as the DIABIMMUNE study (sampled from 2 months of age (Vatanen *et al.*, 2016), and the TEDDY study (Stewart *et al.*, 2018), sampled from 3 months of age), were not directly relevant as they exclusively sampled a different sampling window period (post-neonatal infancy). Although these studies did not sample the neonatal period (first month of life), the caesarean-section babies in these cohorts were also enriched in potential opportunistic pathogens such as *Enterococcus* (Vatanen *et al.,* 2016) and *Clostridium/Clostridium perfringens* (Vatanen *et al*., 2016; Stewart *et al.*, 2018) during the first year of life. Overall, in these cohorts, the differences in the levels of opportunistic pathogens were very small or not statistically significant in babies sampled in post-neonatal infancy period, which is consistent with my observations in the UK babies when sampled in infancy.

3.3.6 Validation of pathogen carriage with culturing and whole-genome sequencing.

Given the prevalent carriage of opportunistic pathogens in the metagenomes of the neonatal gut, I then sought to validate the presence and viability of these pathogens with culturing. This work involved large-scale targeted cultivation of mainly *Enterococcus*, *Klebsiella and Enterobacter* strains using selective culturing media and conditions (see 'Bacterial isolation and whole-genome sequencing' in Methods) on the frozen faecal samples in the BBS biobank.

Overall, I validated the extensive opportunistic pathogen species carriage through culturing, isolation and whole-genome sequencing of 836 strains of putative opportunistic pathogens in the faecal samples of 177 babies (70 vaginally delivered babies and 107 babies delivered by caesarean section; a total of 741 isolates) and 38 mothers (95 isolates, Figure 3.4, Appendices 5-7).

The four most prevalent opportunistic pathogen species (*E. faecalis*, $n = 356$ isolates*; E. cloacae,* $n = 52$ isolates*; K. oxytoca*, $n = 150$ strains and *K. pneumoniae*, $n = 78$ isolates) in this genome collection were further analysed in the context of the public genomes (Supplementary Table 5), including the UK-hospital strain collections (Raven *et al.*, 2016; Moradigaravand *et al.*, 2016; 2017a; 2017b), the gut-microbiota-cultured strains from the Human Gastrointestinal Bacteria Genome Collection (Forster *et al.*, 2019) and the Culturable Genome Reference (Zou *et al.*, 2019), and the environmental strains on the Genome Taxonomy Database (v.86, Parks *et al.*, 2018). This enabled me to perform high-resolution phylogenetic analysis and to delineate the strain-specific carriage of virulence factors and genes associated with antimicrobial resistance (AMR), both of which remain technically non-trivial using coverage-dependent, short-read metagenomic sequencing alone (Forbes *et al.*, 2017; Zaheer *et al.*, 2018; Gweon *et al.*, 2019).

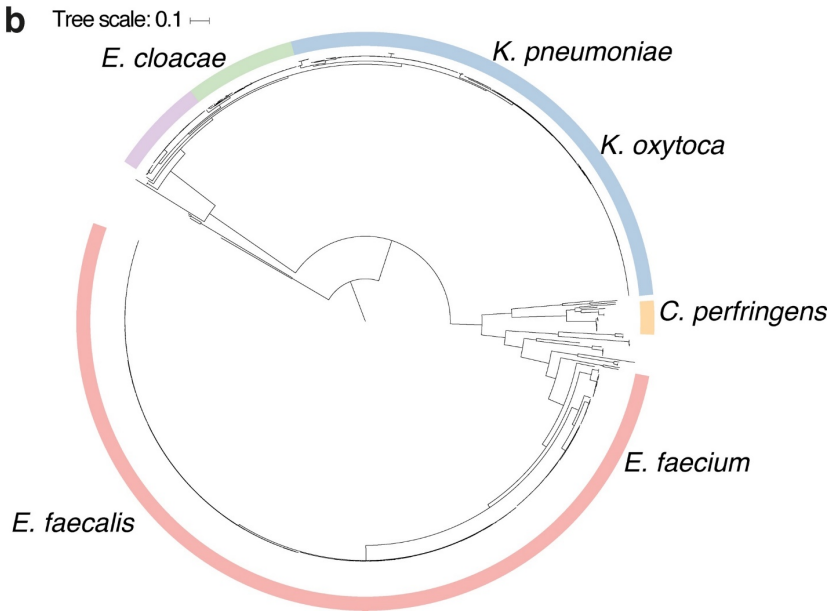

Figure 3.4 Phylogenetic representation of 836 cultured bacterial genomes.

Phylogenetic representation of 836 bacterial isolates cultured from raw faecal samples, including the 6 opportunistic pathogens isolated from 5 major genera: *Enterococcus* spp. (red, $n = 451$ isolates); *Clostridium* spp. (yellow, $n = 24$ isolates); *Klebsiella* spp. (blue, $n = 235$ isolates), *Enterobacter* spp. (green, $n = 52$ isolates) and *Escherichia* spp. (purple, $n = 41$ isolates).

3.3.6.1 Genomic analysis of the *Enterococcus faecalis* strains.

Focusing on the most-prevalent opportunistic pathogen in babies delivered by caesarean section, I analysed the genomes of a diverse population of *E. faecalis* strains from the BBS in the context of publicly available genomes of human and environmental strains of *E. faecalis* (Figure 3.5). 53.9% of the strains in the BBS were represented by 5 major lineages (ST179, ST16, ST40, ST30, ST191), each of which was distributed across vaginally delivered babies and babies delivered by caesarean section (and their mothers) in the three BBS hospitals (Figure 3.6) and across patients with bloodstream infections in UK hospitals. Notably, the BBS strains did not include high-risk UK epidemic lineages that are enriched in multi-drug resistance and virulence (Raven *et al.*, 2016).

Consistent with the phylogenetic placement of strains of the BBS with the human gastrointestinal and environmental strains, these non-epidemic *E. faecalis* strains exhibited comparable levels of carriage of genes related to AMR, although the BBS strains did encode a higher number of virulence factors such as aggregation substance (*EF0485*), surface adhesins (*esp*), hyaluronidase (*EF3023*), and the toxin cytolysin (*cyl*), Figure 3.7a-b). While all *E. faecalis* are intrinsically resistant to cephalosporins (Gilmore *et al.*, 2014) routinely used in IAP and caesarean section, 21.6% (77/356) of the BBS strains also carried genes encoding AMR to aminoglycosides commonly used in enterococcal infections (Figure 3.7c-d). Importantly, no *E. faecalis* from the BBS babies were predicted to carry genes conferring resistance to vancomycin, a clinically significant antimicrobial drug for which the resistant lineages (VREfs) were associated with epidemic outbreaks (Kawalec *et al.*, 2007; Raven *et al.*, 2016); thus indicating the BBS strains were all vancomycin-susceptible *E. faecalis* (VSEfs). Taken together, the lack of phylogenetic clustering by individual BBS hospitals and with known UK epidemic strains, and the non-epidemic level of AMR and virulence gene carriage, indicated that the BBS strains were mostly representative of the non-epidemic lineages circulating in both hospital environments and healthy human populations.

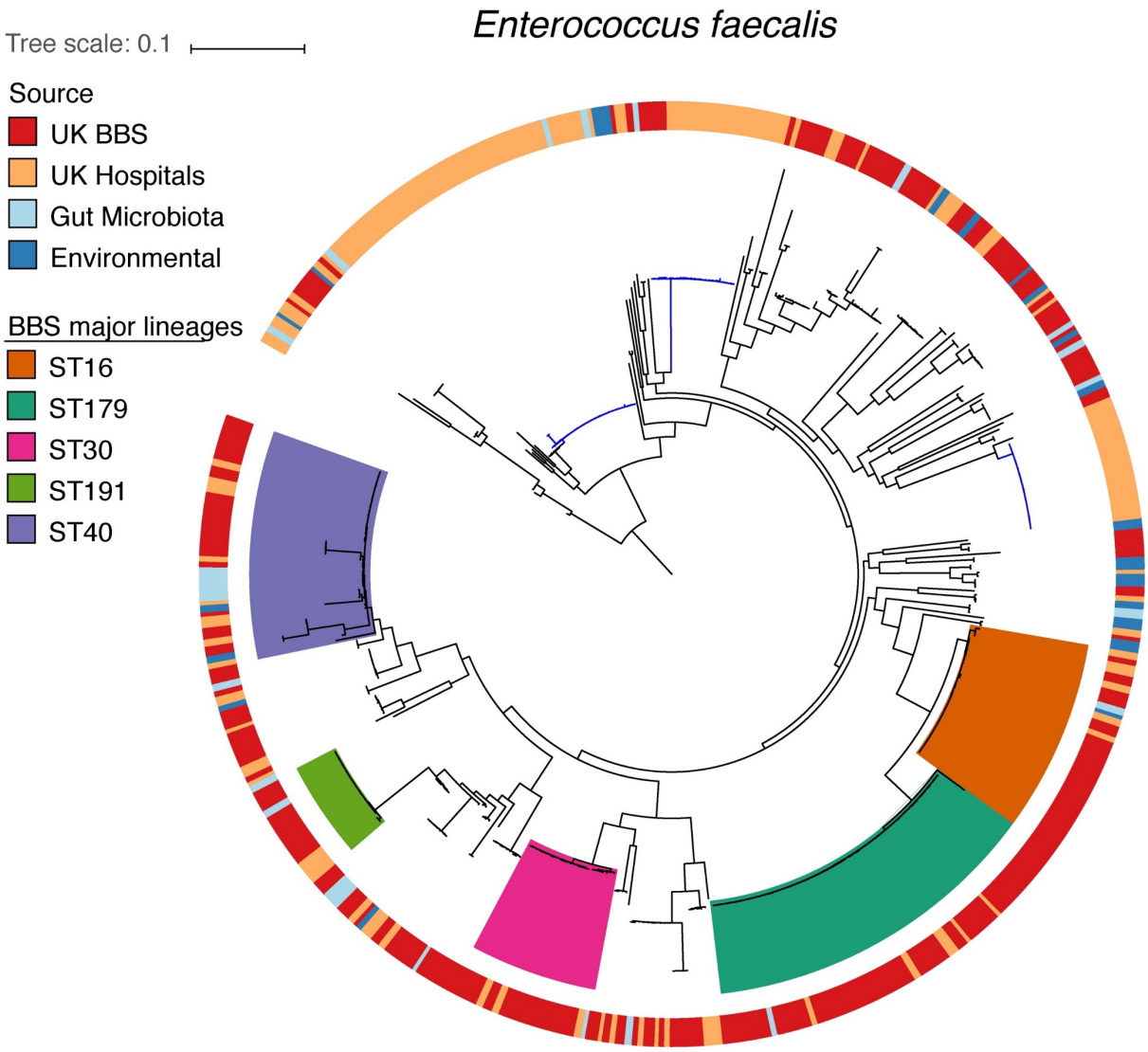

Figure 3.5 Phylogeny of *E. faecalis* strains of the BBS in the context of global genome collection.

Phylogeny of *E. faecalis* strains isolated from the BBS (n = 282 isolates) in the context of public isolates from the UK hospitals (n = 168 isolates) human-gut microbiotas (n = 28 isolates) and environmental sources (n = 27 isolates) with the high-risk UK epidemic lineage branches coloured in blue. Midpoint-rooted maximum-likelihood tree is based on single-nucleotide polymorphisms in 1,656 core genes.

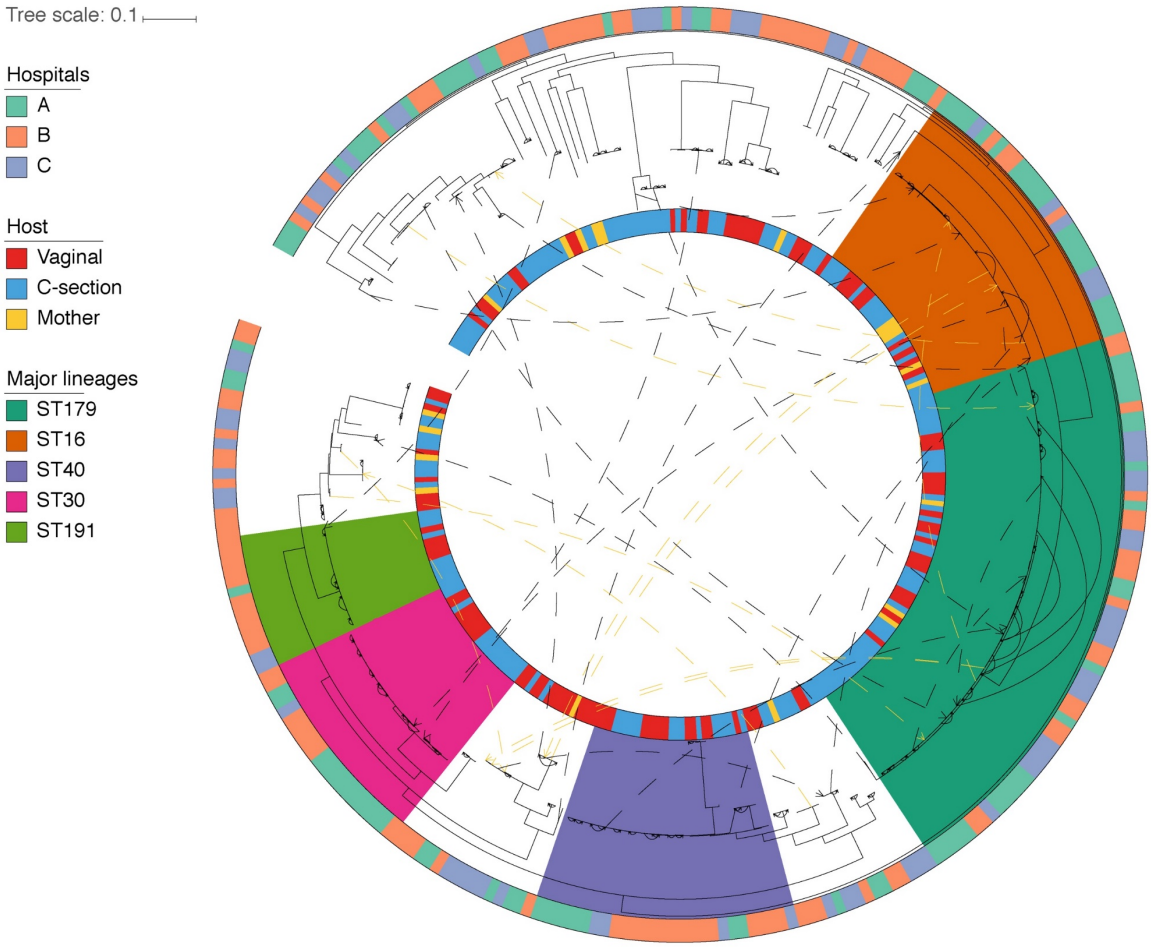

Figure 3.6 Phylogeny and transmission dynamics of *E. faecalis* strains of the BBS.

Phylogenetic tree of *E. faecalis* strains of the BBS ($n = 282$ strains, isolated from 269 faecal samples of 160 subjects). The midpoint-rooted maximum-likelihood phylogeny is based on SNPs in 1,827 core genes. Five major lineages (>10 representatives in the strains of the BBS; ST179, $n = 60$; ST16, $n = 30$, ST40, $n = 27$; ST30, $n = 21$; and ST191, $n = 14$) were identified within UK hospital collections, distributed across three hospitals in this study and with no phylogroup limited to any single hospital. Solid lines between strains indicate intra-subject strain persistence ($n = 92$ strains in 67 babies). Dashed lines indicate phylogenetically distinct strains that were isolated from longitudinal samples ($n = 18$) or mother–baby paired samples (yellow, $n = 10$); arrows indicate the direction of the potential transmission (early-to-later or mother-to-baby). In situations in which multiple identical strains (no SNP difference in species core genome) were isolated from the same faecal sample, only one representative strain was included in the species phylogenetic tree (total number of strains, $n = 356$).

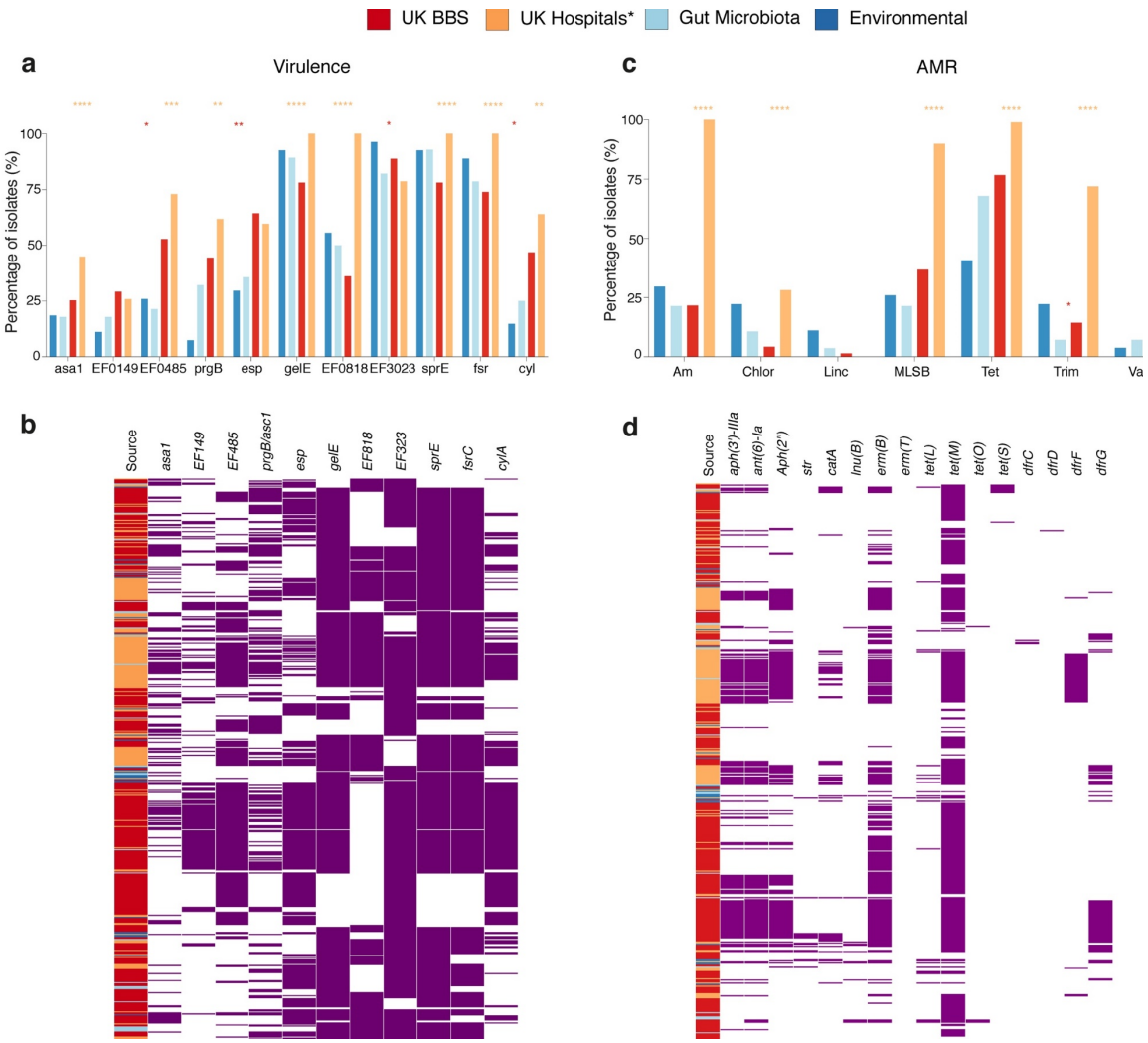

Figure 3.7 Carriage of AMR and virulence genes in *E. faecalis*.

a-d, Prevalence of virulence-related genes (**a**, **b**) and AMR-related genes (grouped by antibiotic class) (**c, d**) detected in the *E. faecalis* strains of the BBS. Significance results shown are coloured according to the group with higher frequency of detected genes, by two-sided Fisher's exact test between groups of the public gut microbiota strains ($n = 28$) versus strains of the BBS ($n = 356$), and strains of BBS versus epidemic strains in UK hospitals ($n = 89$; tree branches coloured blue in Figure 3.4). $^{****}P < 0.0001$, $^{***}P < 0.001$, $^{**}P < 0.01$, $^{*}P < 0.05$. Virulence-related genes: *asa1*, *EF0149*, *EF0485* and *prgB*, aggregation substance; *esp*, enterococcal surface protein; genes that encode exoenzymes: *gelE*, gelatinase; *EF0818* and *EF3023*, hyaluronidase (spreading factor); *sprE*, serine protease; and *fsr*, quorum sensing system; toxin-encoding gene: *cyl*, cytolysin. Genes that were detected across all isolates (*dfrE*, *efrA*, *efrB*, *emeA* and *lsaA*) are not shown. AMR-related genes: Am, aminoglycosides (*aph3''-III*, *ant(6)-Ia*, *aph(2'')* and *str*); Chlor, chloramphenicol (*catA*); Linc, lincosamides (*lnuB*); MLSB, macrolide, lincosamide and streptogramin B (*ermB* or *ermT*); Tet, tetracycline (*tetL*, *tetM*, *tetO* and *tetS*); Trim, trimethoprim (*dfrC*, *dfrD*, *dfrF* or *dfrG*); and Vanc, vancomycin.

3.3.6.2 Genomic analysis of the *Klebsiella* and *Enterobacter* strains.

Similar to *E. faecalis*, the BBS *Enterobacter* and *Klebsiella* strains (both Proteobacteria phylum) also exhibited high-level population diversities with no phylogenetic clustering by individual BBS hospitals (Figure 3.8-3.11). The strains cultured from vaginal and caesarean-section-born babies and mothers were spread across phylogenetically distant lineages and ST groups (Figure 3.9-3.11, Appendix 5), and under-represented in the dominant UK epidemic lineages (*E. cloacae* complex VIII (*E. hormaechei* subsp. *steigerwaltii*), p=0.0043; K. oxytoca KoII, p<0.0001; *K. pneumoniae* KpI, p=0.0059; Fisher's exact test), in line with the epidemiological pattern of these environmental opportunistic pathogens (Moradigaravand *et al.*, 2016; 2017a; 2017b).

Overall, the BBS strain collection included all three major sub-species of *K. pneumoniae* representative of the global (Holt *et al.*, 2015) and UK collection (Moradigaravand *et al.*, 2017a), including the predominant *K. pneumoniae* (KpI), followed by *K. quasipneumoniae* (KpII), and *K. variicola* (KpIII), Figure 3.11). Likewise, all four major phylogenetic groups of *K. oxytoca* (KoI, KoII, KoVI, and KoV, Moradigaravand *et al.*, 2017b), and nine out of eleven *E. cloacae* complex genovars in the UK collection (Moradigaravand *et al.*, 2016) were represented by the BBS strain collection (Figure 3.9-3.11).

Furthermore, the BBS strains also showed levels of gene carriage associated with AMR and virulence that were indicative of non-epidemic lineages that circulate in hospital environments and healthy populations, rather than epidemic lineages that are hypervirulent and enriched for extended-spectrum β-lactamases (Figure 3.12). While these Gram-negative opportunistic pathogens are also known to exhibit intrinsic resistance to penicillins and most cephalosporins used in IAP and caesarean section, genes encoding for AmpC, class A and extended-spectrum beta-lactamases (ESBL) were detected in most of the BBS *E. cloacae* (bla_{ACT}, 88.5%), *K. oxytoca* (bla_{OXY}, 100%) and *K. pneumoniae* (bla_{SHV}, 82.1%) strains, respectively (Figure 3.12

a-b). With the exception of tetracycline resistance enriched in the BBS *K. oxytoca*, the prevalence of AMR and virulence gene in the BBS strains are mostly representative of the non-epidemic lineages circulating in hospital environments and healthy populations, rather than selective colonisation of the hypervirulent and ESBL-enriched (bla_{SHV}, $bla_{CTX\text{-}M}$, bla_{TEM}) epidemic lineages (Figure 3.12). Overall, these results were consistent with the phylogenetic under-representation of epidemic lineages (from UK hospital collections) in the BBS collection, and also in agreement with my previous observations with *E. faecalis*.

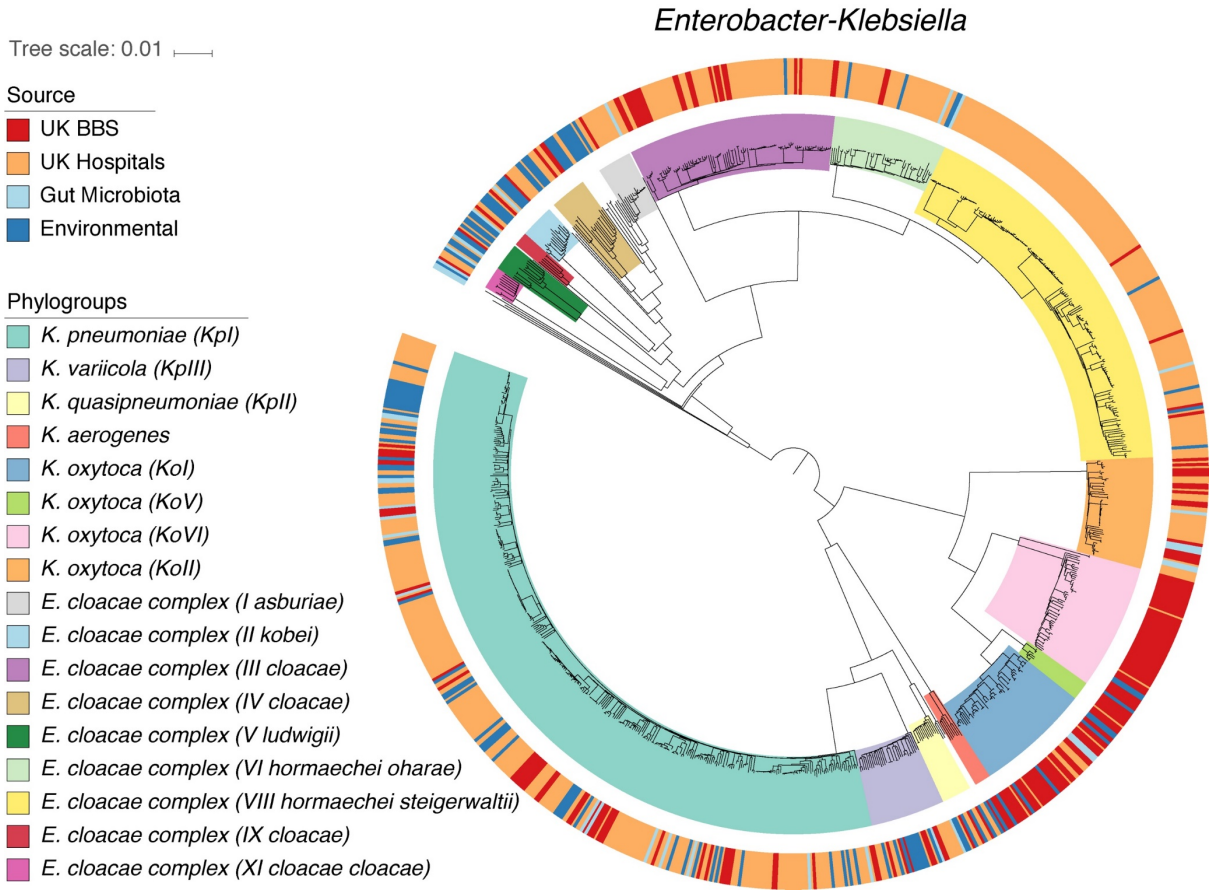

Figure 3.8 Phylogeny of *Enterobacter–Klebsiella* complex strains of the BBS in the context of global genome collection.

Diverse strain populations of *Enterobacter–Klebsiella* complex strains in the BBS collection ($n = 202$ isolates in the context of the UK hospital ($n = 604$), human-gut microbiota ($n = 37$) and environmental strains ($n = 120$).

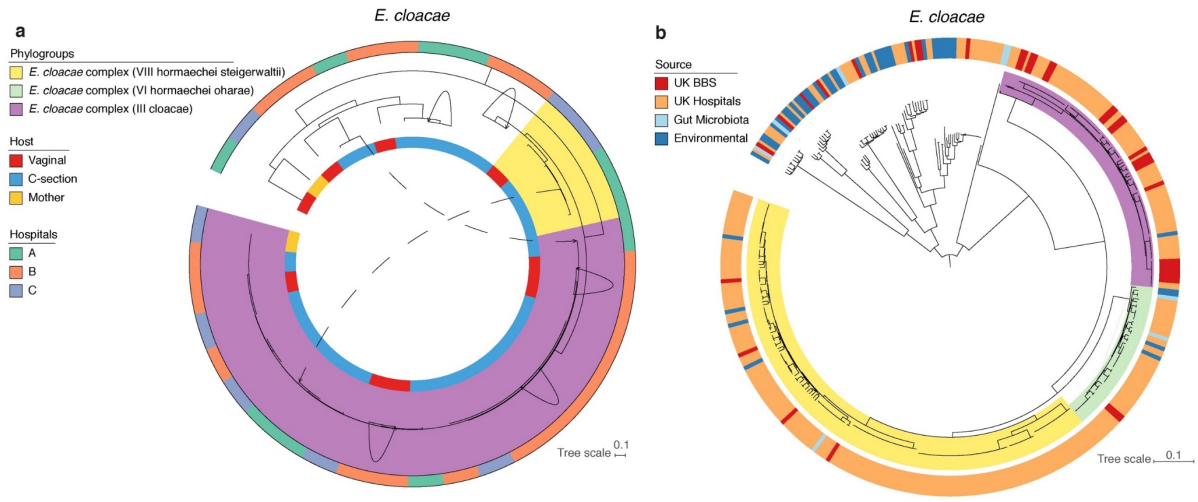

Figure 3.9 Phylogenies of *E. cloacae* strains of the BBS.

a–**b,** Midpoint-rooted core-genome maximum-likelihood trees of *E. cloacae* complex strains isolated in this study **(a)** and in the context of public genomes **(b)**. **a,** Number of strains of *E. cloacae* ($n = 37$, isolated from 37 faecal samples of 30 subjects, 1,861 core genes). Solid lines between strains indicate intra-subject strain persistence (*E. cloacae*, $n = 5$ strains in 5 babies. Dashed lines indicate phylogenetically distinct strains isolated from longitudinal samples (*E. cloacae*, $n = 2$ strains in 2 individuals); arrows indicate the direction of potential transmission (early-to-later samples). In situations in which multiple identical strains (no difference in SNPs in species core genome) were isolated from the same faecal sample, only one representative strain was included in the species phylogenetic tree (number of non-redundant BBS strains: *E. cloacae*, n = 52). **b,** The main phylogroups identified with UK hospital collections are shown (*E. cloacae*, III and VIII); these were distributed across three hospitals in this study, with no phylogroup limited to any single hospital. The number of public genomes included in the phylogenetic analysis of *E. cloacae* (UK hospitals, $n = 314$; gut microbiota, $n = 8$; environmental sources, $n = 43$; 1,484 core genes).

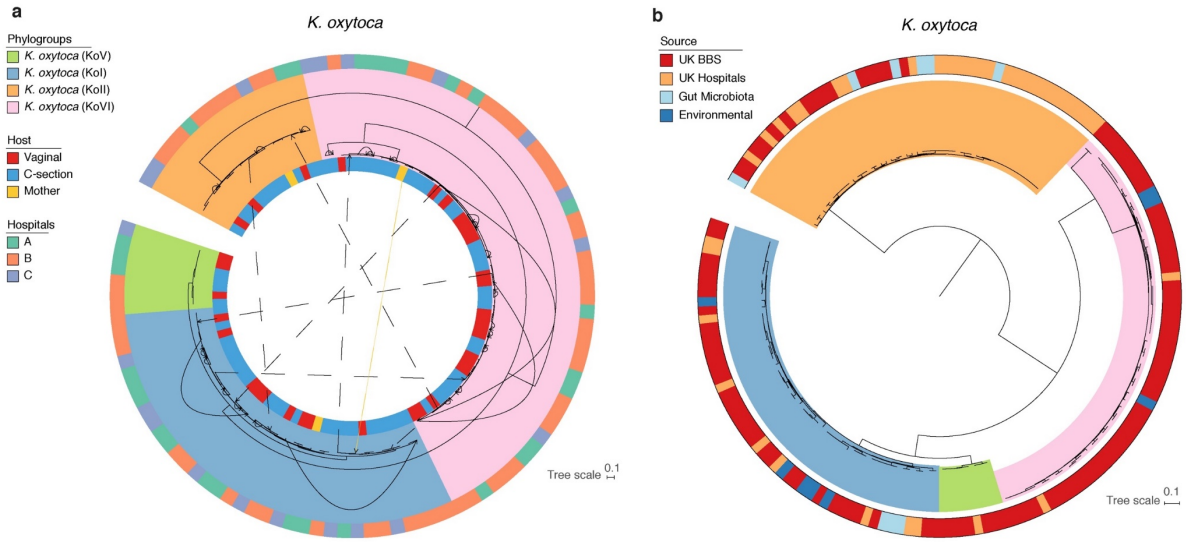

Figure 3.10 Phylogenies of *K. oxytoca* strains of the BBS.

a–**b,** Midpoint-rooted core-genome maximum-likelihood trees of *K. oxytoca* strains isolated in this study **(a)** and in the context of public genomes **(b). a,** Number of strains of *K. oxytoca* (n = 107, isolated from 90 faecal samples of 62 subjects, 2,910 core genes). Solid lines between strains indicate intra-subject strain persistence (*K. oxytoca*, n = 25 strains in 18 babies. Dashed lines indicate phylogenetically distinct strains isolated from longitudinal samples (*K. oxytoca*, n = 7 strains in 6 subjects); arrows indicate the direction of potential transmission (early-to-later samples). In situations in which multiple identical strains (no difference in SNPs in species core genome) were isolated from the same faecal sample, only one representative strain was included in the species phylogenetic tree (number of non-redundant BBS strains: *K. oxytoca*, n = 150). **b,** The main phylogroups identified with UK hospital collections are shown (*K. oxytoca*, KoI, KoII, KoV and KoVI); these were distributed across three hospitals in this study, with no phylogroup limited to any single hospital. The number of public genomes included in the phylogenetic analysis of *K. oxytoca* (UK hospitals, n = 40; gut microbiota, n = 9; environmental sources, n = 8; 3,399 core genes).

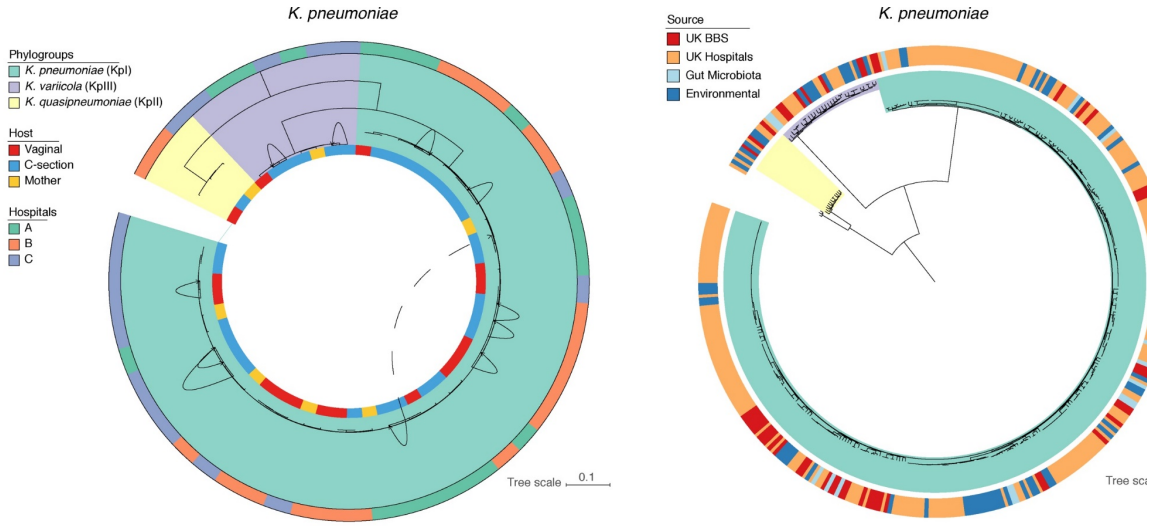

Figure 3.11 Phylogenies of *K. pneumoniae* strains of the BBS.

a–**b,** Midpoint-rooted core-genome maximum-likelihood trees of *K. pneumoniae* strains isolated in this study **(a)** and in the context of public genomes **(b)**. **a,** Number of strains of *K. pneumoniae* (a) ($n = 53$, isolated from 47 faecal samples of 35 subjects, 3,471 core genes). Solid lines between strains indicate intra-subject strain persistence (*K. pneumoniae*, $n = 11$ strains in 8 babies. Dashed lines indicate phylogenetically distinct strains isolated from longitudinal samples ($n = 1$ strain in 1 individual); arrows indicate the direction of potential transmission (early-to-later samples). In situations in which multiple identical strains (no difference in SNPs in species core genome) were isolated from the same faecal sample, only one representative strain was included in the species phylogenetic tree (number of non-redundant BBS strains: *K. pneumoniae*, $n = 78$). **b,** The main phylogroups identified with UK hospital collections are shown (*K. pneumoniae*, KpI, KpII and KpIII); these were distributed across three hospitals in this study, with no phylogroup limited to any single hospital. The number of public genomes included in the phylogenetic analysis of *K. pneumoniae* (UK hospitals, $n = 250$; gut microbiota, $n = 17$; environmental sources, $n = 66$; 2,510 core genes).

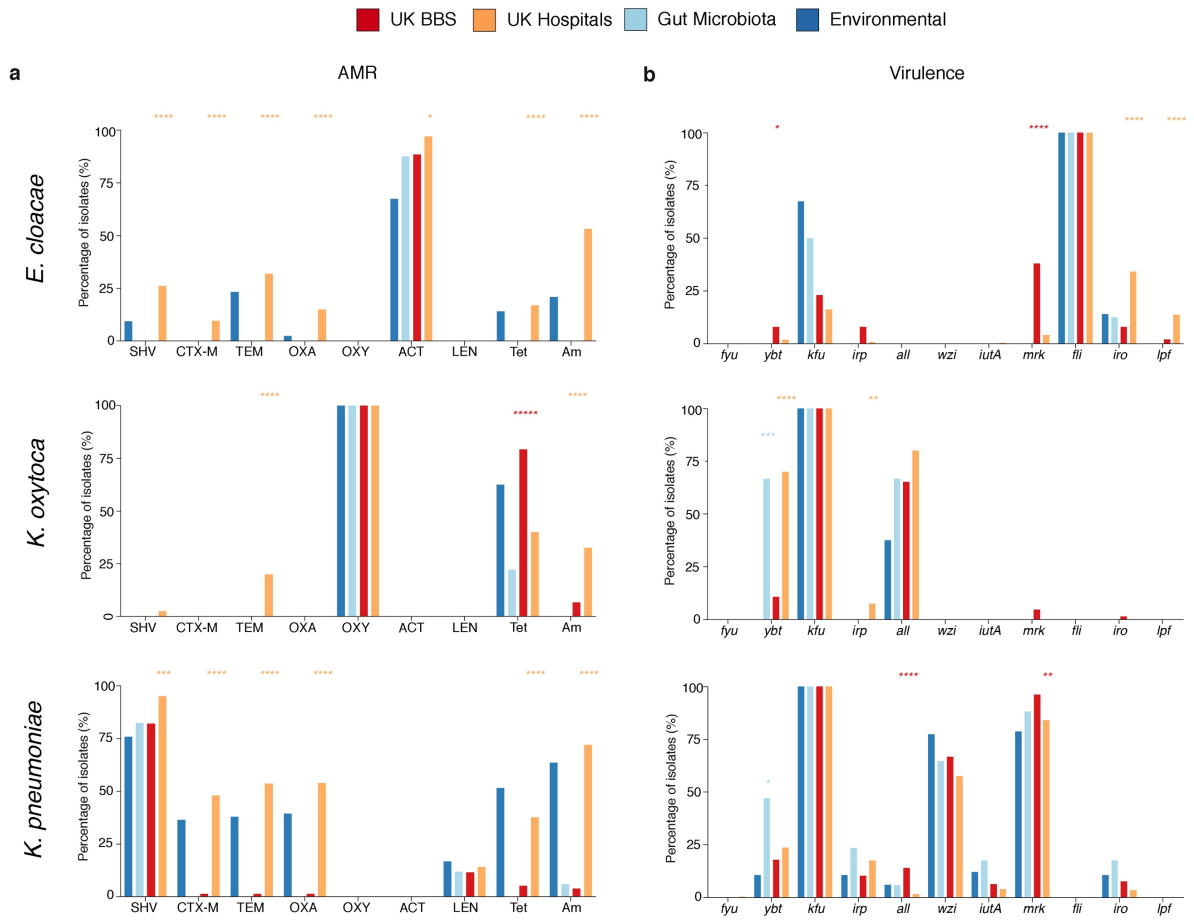

Figure 3.12 Frequency of AMR and virulence genes detected in *Klebsiella* and *Enterobacter* strains.

a–**b**, Frequency of isolates for putative AMR-related **(a)** and virulence-related genes (grouped by antibiotic class) **(b)** that are most-frequently detected in strains of the UK hospital collection of *E. cloacae*, *K. oxytoca* and *K. pneumoniae*. Significance results shown are coloured according to the group with higher frequency of detected genes, by two-sided Fisher's exact test between groups of the public gut microbiota strains (*E. cloacae*, $n = 8$; *K. oxytoca*, $n = 9$; and *K. pneumoniae*, $n = 17$) versus strains in the BBS (*E. cloacae*, $n = 52$; *K. oxytoca*, $n = 150$; and *K. pneumoniae*, $n = 78$), and strains in the BBS versus strains in UK hospitals (*E. cloacae*, $n = 314$; *K. oxytoca*, $n = 40$; *K. pneumoniae*, $n = 250$). ****$P < 0.0001$, ***$P < 0.001$, **$P < 0.01$, *$P < 0.05$. AMR-related genes: extended-spectrum β-lactamases, SHV (bla_{SHV}), CTX-M ($bla_{CTX\text{-}M}$) and TEM (bla_{TEM}); other β-lactamases, OXA (bla_{OXA}), OXY (bla_{OXY}), ACT (bla_{ACT}) and LEN (bla_{LEN}); Tet, tetracycline (*tetA* and *tetR*); Am, aminoglycosides (*aac(3)*, *aac(6')*, *aad* and *str*). Virulence-related genes: iron acquisition, *fyu*; yersiniabactin, *ybt*; iron transporter permease, *kfu*; iron regulatory proteins, *irp*; allatonin metabolism, *all*; capsule, *wzi*; aerobactin siderophore receptor, *iutA*; fimbriae and biofilm formation, *mrk*; flagella biosynthesis, *fli*; siderophore production, *iro*; and fimbrial chaperones, *lpf*. Genes detected across all isolates are not shown.

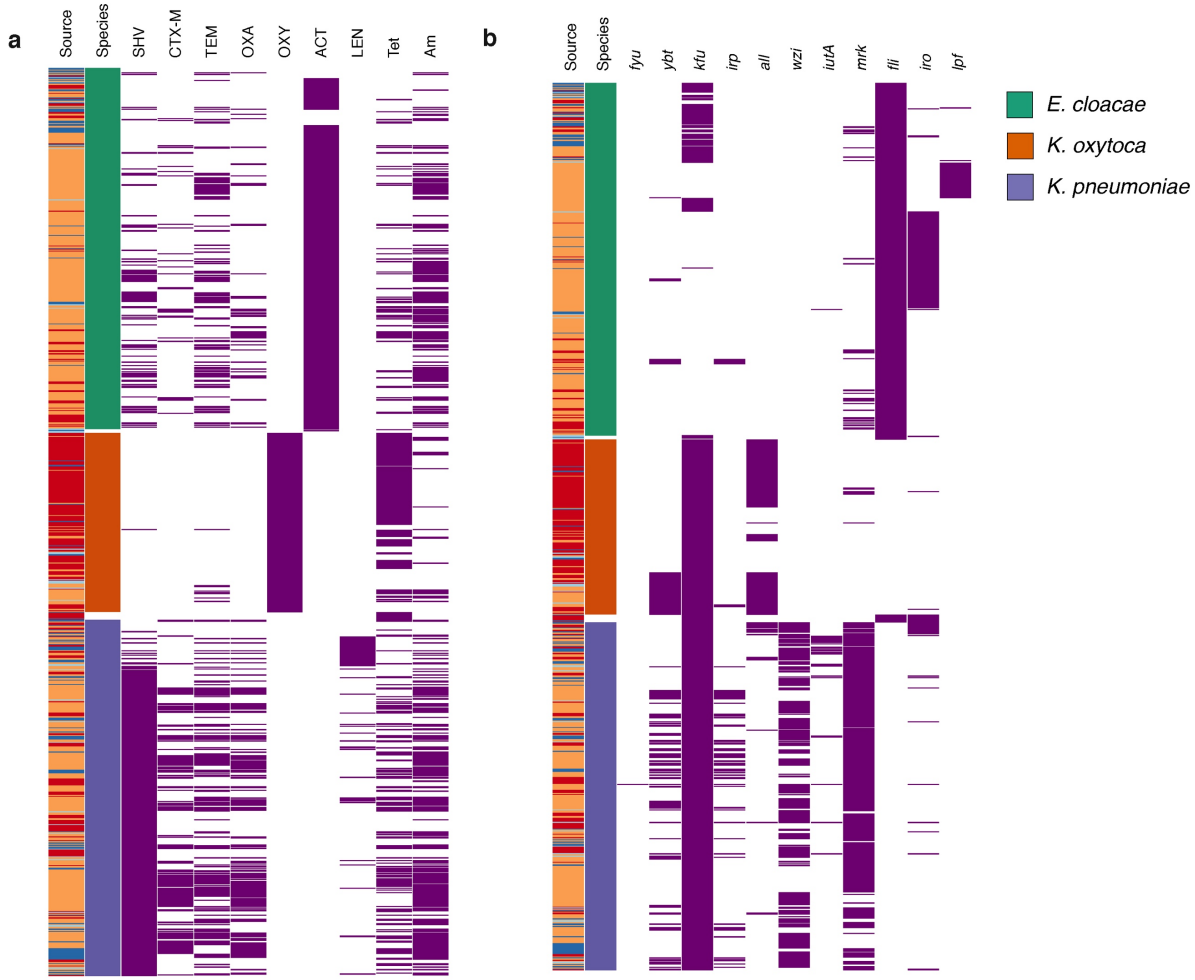

Figure 3.13 Heatmaps of AMR and virulence genes detected in *Klebsiella* and *Enterobacter* strains.

a–**b**, Heatmaps of isolates for putative AMR-related **(a)** and virulence-related genes (grouped by antibiotic class) **(b)** that are most-frequently detected in strains of the UK hospital collection of *E. cloacae* (green), *K. oxytoca* (red) and *K. pneumoniae* (blue). Significance results shown are coloured according to the group with higher frequency of detected genes, by two-sided Fisher's exact test between groups of gut microbiota (*E. cloacae*, $n = 8$; *K. oxytoca*, $n = 9$; and *K. pneumoniae*, $n = 17$) versus strains in the BBS (*E. cloacae*, $n = 52$; *K. oxytoca*, $n = 150$; and *K. pneumoniae*, $n = 78$), and strains in the BBS versus strains in UK hospitals (*E. cloacae*, $n = 314$; *K. oxytoca*, $n = 40$; *K. pneumoniae*, $n = 250$). ****$P < 0.0001$, ***$P < 0.001$, **$P < 0.01$, *$P < 0.05$. AMR-related genes: extended-spectrum β-lactamases, SHV (bla_{SHV}), CTX-M ($bla_{CTX\text{-}M}$) and TEM (bla_{TEM}); other β-lactamases, OXA (bla_{OXA}), OXY (bla_{OXY}), ACT (bla_{ACT}) and LEN (bla_{LEN}); Tet, tetracycline (*tetA* and *tetR*); Am, aminoglycosides (*aac(3)*, *aac(6')*, *aad* and *str*). Virulence-related genes: iron acquisition, *fyu*; yersiniabactin, *ybt*; iron transporter permease, *kfu*; iron regulatory proteins, *irp*; allatonin metabolism, *all*; capsule, *wzi*; aerobactin siderophore receptor, *iutA*; fimbriae and biofilm formation, *mrk*; flagella biosynthesis, *fli*; siderophore production, *iro*; and fimbrial chaperones, *lpf*. Genes detected across all isolates are not shown.

3.3.6.3 Rare transmission of maternal opportunistic pathogen strains.

To detect potential transmission of opportunistic pathogen strains from mothers to their babies, I performed analysis on the paired maternal and neonatal strains in both cultured whole-genomes and metagenomes. Of the four opportunistic pathogens with isolate genomes, in a majority of the babies (78.53%, 95% CI 66.51-90.54%) carrying one of the four opportunistic pathogens, identical strains were isolated from the longitudinal samples of the same individual, indicating stable colonisation of a single strain. In contrast, no identical strains were isolated from mother-baby dyads that would otherwise indicate a direct route of maternal transmission (phylogenetically distant maternal-neonatal paired-strains found in *E. faecalis*, $n = 10$, Figure 3.6; *K. oxytoca*, $n = 1$, Figure 3.10a).

This result corroborates the metagenomic strain transmission analysis (Section 2.3.6), in which four opportunistic pathogen species (*E. faecalis,* $n = 7$*; E. faecium*, $n = 2$; *K. oxytoca,* $n = 2$, *K. pneumoniae,* $n = 1$) had a significantly lower transmission rate (57.14%) compared to the known typical maternally-transmitted *Bacteroides/Parabacteroides* species (93.35%, Fisher's exact test, $p<0.0001$, Appendix 3). Furthermore, the total number of transmissions of opportunistic pathogens (9 transmissions, 12 non-transmissions) detected in this study represented only a tiny proportion (~2%) of the total neonatal transmissions ($n = 657$) and typable sample-species pairs ($n = 995$) across all analysed species, indicating that maternal transmission of the opportunistic pathogen species was very rare overall. However, this analysis was limited to <10% of the total mother-neonate pairs ($n = 178$) due to rare and very low-level carriage in healthy adults with sufficient sequencing coverage required by metagenomic strain transmission analysis.

Taken together, although I did detect cases of putative strain transmission of the opportunistic pathogens between mothers and babies, the overall rare occurrences detected in metagenomes and isolate genomes and insignificant scale of maternal transmission did not support an apparent maternal origin of opportunistic pathogens.

3.4 Conclusions

In this chapter, I reported the extensive and frequent colonisation of several opportunistic pathogen species in the gut metagenomes of the babies delivered by caesarean section, and to a lesser extent in the vaginally delivered babies with the low-*Bacteroides* profile, and also in those who were not breastfed during the neonatal period. The opportunistic pathogen carriage in very early life had previously been widely reported in preterm hospitalised babies, but overlooked in full-term cohort studies due to insufficient statistical power. By sampling the full-term healthy babies in the very same early window, this work extended the very similar opportunistic pathogen colonisation pattern to full-term, hospital-born neonates with those delivered by caesarean section being predisposed to frequent opportunistic pathogen carriage.

This surprising finding was experimentally validated through matched large-scale culturing and whole-genome sequencing of over 800 bacterial strains cultivated from raw faecal samples. The virulence and AMR gene analyses agreed with the phylogenetic placement of the BBS strains with the human gastrointestinal and environmental strains and the phylogenetic under-representation of epidemic lineages in the BBS collection, suggesting that the BBS strains were mostly representative of the non-epidemic lineages circulating in hospital environments and healthy populations, rather than selective colonisation of the hypervirulent and multi-drug resistant epidemic lineages.

Interestingly, the observations that the BBS *E. faecalis* strains encoded a higher number of virulence factors (aggregation substance, surface adhesins, hyaluronidase, and the toxin cytolysin) compared to the other non-epidemic strains; and the BBS *K. oxytoca* strains were enriched in tetracycline resistance genes, suggest that these more pathogenic BBS strains might be better adapted to the hospital environment, in comparison to the true commensal strains in healthy carriers. Given that virulence and AMR were predicted *in silico* in the current study,

future validation experiments are needed to test if the virulence and AMR genes are indeed functional.

Asymptomatic carriage of opportunistic pathogens had recently been shown to be the main source of hospital-associated infections (Gorrie *et al.*, 2017; Tamburini *et al.*, 2018). Given the previous isolation of the major BBS lineages in hospitalised patients with bloodstream infections, and their AMR and virulence capabilities, any level of opportunistic pathogen carriage represents a considerable risk of opportunistic infections, especially for the babies delivered by caesarean section who have a high prevalence (83.7%) of carriage.

Although there was insufficient evidence from metagenomics and the whole-genome sequencing of cultured isolates to rule out a maternal origin for the opportunistic pathogens, the absence of lineage-specific colonisation suggests that exposure to the hospital environment was the primary factor that drives colonisation by opportunistic pathogens in the babies of the BBS. Whilst this study was not designed for the retrospective sampling of the hospital environmental sources, opportunistic pathogens are frequently found in hospital environments; hospital-born babies have been shown to carry the same bacteria that are present in the operating rooms (Shin *et al.*, 2015) and neonatal intensive care units (Brooks *et al.*, 2014).

Taken together, the neonatal gut microbiota associated with early-life perturbation events could act as a reservoir of opportunistic pathogens circulating in healthcare and hospital environments, many of which are known key spreaders of clinically important AMR genes (Wyres, Holt, 2018). Subject to the selection pressure of postnatal antibiotics, persistence and enrichment of these multidrug-resistant pathogens represent a significant risk of AMR dissemination in gut microbial communities and opportunistic infections in individuals during a high-risk period (<1 year old, Cassini *et al.*, 2019). This work emphasises the underappreciated importance of the local bacterial species pool in hospital and healthcare environments in seeding the gut microbiota of hospital-born babies.

Chapter 4: Genomic blueprint of the neonatal gut microbiota

4.1 Introduction and aims

Taxonomic profiling of large-scale shotgun metagenomic datasets (Lloyd-Price *et al.*, 2017; Vatanen et al., 2018; Lloyd-Price *et al.*, 2019) typically utilise the fast and cost-effective read mapping-approach that relies heavily on the coverage and quality of reference genome databases (Quince *et al.*, 2017). Recent breakthroughs from large-scale microbial culturing efforts (Browne *et al.*, 2016; Lagier *et al.*, 2016) and tremendous metagenome assembly efforts had led to a substantial expansion of high-quality, human gut microbiota reference cultured isolate (Forster *et al.*, 2019; Zou *et al.*, 2019) and metagenome-assembled (Pasolli *et al.*, 2019; Almeida *et al.*, 2019b; Nayfach *et al.*, 2019) genomes, many of which were novel genomes that had not been previously cultivated. These important genomic catalogues have significantly enhanced the taxonomic classification of reference-based, gut metagenome analyses, with improved resolution of taxonomic assignment now readily achievable at species and strain-level (Forster *et al.*, 2018; Pasolli *et al.*, 2019).

The BBS metagenomes in this study were classified using a human gut microbiota-specific, high-quality reference database consisting of bacterial genomes in the Human Gastrointestinal Microbiota Genome Collection (HGG) (Forster *et al.*, 2018), which had been internally assembled and curated in the host lab over the course of this study. The HGG database, though it covers a much smaller number of bacterial genomes (n = 1,354) than the RefSeq (bacterial, archaeal, and viral genomes, n = 96,071), performed remarkably well in achieving substantially greater metagenomic classification results than the RefSeq MiniKraken database, as evaluated by the proportion of Kraken-classified sequences (Figure 4.1a). Nearly 90% of the neonatal gut metagenomes representing the majority of the BBS

dataset were readily classifiable using either the HGG (89.0%, 95CI% 88.3-89.6%) or RefSeq (87.1%, 95CI% 86.3-87.3%) MiniKraken database (Figure 4.1b).

These results indicated that majority of the neonatal and infant gut microbiotas were represented by known, cultivated bacteria archived in the HGG and RefSeq, which were both suitable choices for the taxonomic classification of early life gut metagenomic data. However, between 11.0% (neonatal) and 28.3% (adult) of the gut microbiota remained unclassified by a high-quality reference genome database such as HGG, representing unexplored microbial diversity in downstream analyses. Given that the HGG reference database only included cultivated bacterial genomes, sequences matched to any uncultivated bacterial, archaeal, fungal and viral sequences potentially present in a metagenome would be designated as unclassified sequences.

Therefore, the primary objective of this study was to assess the unexplored prokaryotic, eukaryotic and viral diversity in the remaining, unclassified metagenomic sequences (mean 12.9%, 95% CI 12.4-13.5%, Figure 4.1a). I aimed to generate and characterise a comprehensive genomic blueprint of the BBS gut microbiotas by performing reference-free, metagenome assembly. This process involved *de novo* assembly of raw metagenomic reads into contigs, which were then grouped into bins on the basis of sequencing coverage and tetranucleotide frequency, thereby enabling the recovery of potential genomes, termed metagenome-assembled genomes (MAGs). This approach had recently been applied to multiple large-scale metagenomic assembly studies, resulting in the recovery and discovery of hundreds of thousands of genomes and novel microbial species from the human microbiota (Pasolli *et al.*, 2019; Almeida *et al.*, 2019b; Nayfach *et al.*, 2019).

I hypothesised that such a cohort-specific microbiota genome catalogue would yield substantial improvements in the taxonomic classification that would be unmatched by existing reference genomes alone, and could therefore be an essential step to enable assessment of the entirety of the gut microbiota in population-based cohorts.

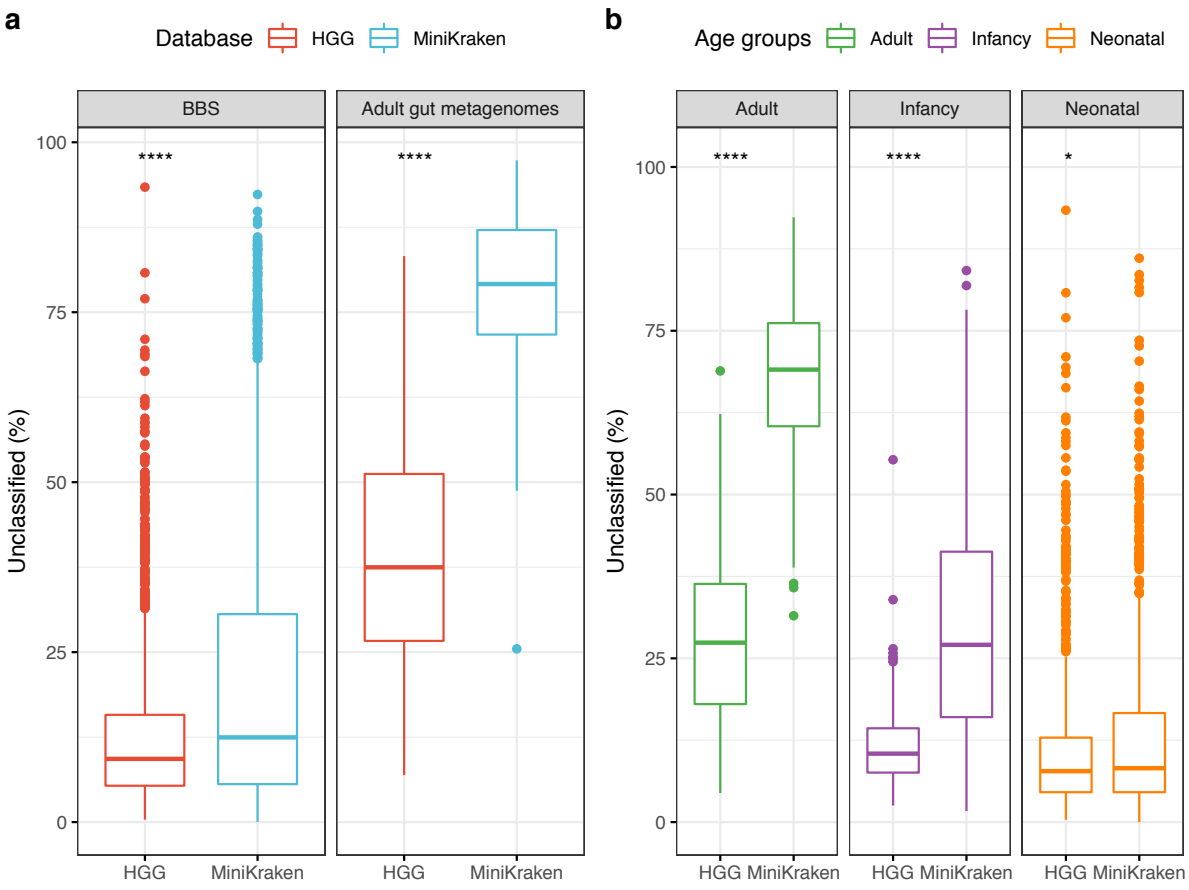

Figure 4.1 The unclassified gut microbiota missing in the reference genome database.

a, Significantly lower proportion of the BBS gut metagenomes (*n* = 1,679) were left unclassified by Kraken using the HGG database (mean 12.9%, 95% CI 12.4-13.5%, red), in comparison to using MiniKraken (RefSeq, blue) database (mean 21.7%, 95% CI 20.65-22.76%). The difference in classifiable proportion as a result database choice is more substantial for the adult gut metagenomes (*n* = 100 randomly selected from ENA) with more complex communities, with a similar pattern also observed within the BBS dataset (**b**). Number of samples in the three age groups: adult (*n* = 175, green), infancy (*n* = 302, purple), neonatal (*n* = 1,202, orange). Statistical comparisons between group means were performed by two-sided Wilcoxon rank-sum tests with significance indicated (* p<0.01, ** p<0.001, *** p<0.0001, **** p<0.00001).

4.2 Materials and methods

4.2.1 Databases for metagenomic classification benchmarking

To benchmark the metagenomic classification performance of HGG, with the BBS and public datasets, a set of 100 public, healthy, adult gut metagenomes were randomly selected and retrieved from the EBI Metagenomics (MGnify) data portal queried based on criteria 'adult', 'healthy' and 'gut' (Appendix 7). To assess how the HGG database classification performance compares with the public genome database (e.g. RefSeq) commonly used in the research community, the MiniKraken database was downloaded from the Kraken website. This database was constructed from the entire RefSeq genome collection (release 84 as of Oct. 18, 2017), including complete bacterial, archaeal, and viral genomes (n = 96,071).

To place the classification performance of the BBS MAGs collection in context, two public, human gut microbiota-derived genome collections were included for Kraken classification benchmarking. These included 1,952 unclassified metagenomic species (UMGS) genomes derived from public gut metagenomes (Almeida *et al.*, 2019b), and 1,520 Culturable Genome Reference (CGR) genomes derived from cultured isolates (Zou *et al.*, 2019). These genome assemblies were downloaded from the ENA using accession numbers ERP108418 and PRJNA482748, respectively.

The Kraken databases were constructed using default parameters and NCBI species taxid of RefSeq and Genbank genomes including the representative genomes of known MAG species (based on the closest ANI distance within a species cluster defined by 95% ANI). For a novel MAG genome and species, the taxon ID was taken from its lowest taxonomic rank in the Genome Taxonomy Database (GTDB) taxonomy. Metagenomic-predicted, novel viral populations could not be assigned NCBI taxonomy ID and were therefore excluded from the Kraken database.

4.2.2 *De novo* metagenome assembly and binning

Quality-controlled, raw paired-end reads from each sample were first assembled with SPAdes v3.13.1(Bankevich *et al.*, 2012) with option *–meta* (Nurk *et al.*, 2017). Unassembled reads were then filtered out by mapping raw reads back to metaSPAdes-assembled contigs using bwa-mem v0.7.17 (Li, Durbin, 2010), followed by re-assembly with MEGAHIT v1.2.4 (Li *et al.*, 2015) using default parameters. Subsequently, the metaSPAdes and MEGAHIT assemblies were combined, sorted, and short contigs (<1,500 bp) removed. The resulting assemblies were then independently binned with MetaBAT 2 v2.13 (Kang *et al.*, 2015; 2019), MaxBin2 v2.2.4 (Wu *et al.*, 2014; 2016) and CONCOCT v0.4 (Alneberg *et al.*, 2014) using default parameters and a minimum contig length threshold of 1,500 bp (option *--minContig* 1500). Depth of contig coverage required for the binning was inferred by mapping the raw reads back to their assemblies with bwa-mem v.0.7.17 and then calculating the corresponding read depths of each individual contig with samtools v1.5 (Li *et al.*, 2009) (‘*samtools view -Sbu’* followed by ‘*samtools sort*’) together with the *jgi_summarize_bam_contig_depths* function from MetaBAT 2.

Thereafter, individual bin sets produced by three binning programs were consolidated to a refined bin set consisting of the best version of each bin based on most optimal genome completion and contamination metrics among of all 7 versions of hybridised bin sets (MetaBAT 2, MaxBin2, CONCOCT , MetaBAT 2 + MaxBin2, MetaBAT 2 + CONCOCT, MaxBin2 + CONCOCT, MetaBAT 2 + MaxBin2 + CONCOCT) sets as estimated by CheckM v1.0.7 (Parks *et al.*, 2015), using metaWRAP’s (v1.2) *bin_refinement* pipeline (Uritskiy *et al.*, 2018).

Genome bins were classified into high-quality (HQ) MAGs based on the criteria defined by a standard of ≥ 90% completeness and ≤5% contamination (Bowers *et al.*, 2017) as determined by CheckM’s *lineage_wf* workflow. The quality score (QS) of each MAG was calculated as the level of completeness − 5 × contamination (Parks *et al.*, 2017).

4.2.3 Taxonomic classification of prokaryotic genomes

High-quality bacterial and archaeal MAGs, as evaluated by CheckM, were subjected to taxonomic classification based on the reference taxonomy and genomes of the Genome Taxonomy Database (GTDB, release 89) using GTDB-tk v0.3.0 (Chaumeil *et al.*, 2019). The GTDB-tk classify workflow takes account both the ANI distance and topological placement of the query genome in relation to the reference genomes in the GTDB. Briefly, 120 bacterial or 122 archaeal ubiquitous single-copy marker genes (Parks *et al.*, 2017) were called from query genomes using Prodigal v2.6 (Hyatt *et al.*, 2012), followed by multiple sequence alignment (MSA) of all query and reference marker genes using HMMER v3.1 (Eddy, 2011). Columns in the MSA with >50% gaps or with a single amino acid spanning <25% or >95% of taxa are removed, resulting to MSAs of 41,155 bacterial or 32,675 archaeal amino acids, respectively. In order to reduce computational requirements, 42 amino acids per marker were randomly selected from the remaining columns. Subsequently, a concatenation of the MSA of 5040 (bacterial) or 5124 (archaeal) amino acids was used to infer the maximum-likelihood phylogenetic placement of each genome in the GTDB reference tree, using pplacer v1.1 (Matsen *et al.*, 2010). Once a query genome is placed within a defined genus, the whole-genome ANI between the query genome and all GTDB reference genomes within the that genus are calculated with FastANI (Jain *et al.*, 2018) v1.1. By default, a query genome is assigned to the same species as its closest intra-genus reference genome if the ANI between the genomes is within the species ANI circumscription threshold (i.e. 95% for most species) and the query alignment fraction is ≥ 0.60, else it is considered a novel species of the given genus. When ANI species assignment was not congruent with its maximum-likelihood phylogenetic placement, usually for species comprising closely related genomes, species assignment was based solely on the calculated ANI and alignment fraction (AF) with a reference genome, in accordance to the species assignment guidelines implemented in the GTDB r89 (https://gtdb.ecogenomic.org/faq). In circumstances when a potentially 'novel' query genome

could not be placed to any existing genus in the GTDB reference tree and that ANI calculation was not applicable, its taxonomic classification is fully defined by topology (phylogenetic placement in the reference tree), and if applicable, using the relative evolutionary divergence (RED) values (Parks *et al.*, 2018). A 'novel' genome that could not be placed in a genus would therefore be considered a novel genus or family in accordance to its maximum-likelihood topology in the GTDB taxonomy. All MAGs in this study were taxonomically labelled according the nomenclature used the in GTDB taxonomy, including those that might not have been officially adopted by the International Code of Nomenclature of Prokaryotes (Parker *et al.*, 2019).

A *de novo*, reference-free phylogenetic tree of the query genomes (high-quality bacterial or archaeal MAGs) was constructed using the full-length concatenated MSA of 120 bacterial or 122 archaeal single-copy marker genes using FastTree (Price *et al.*, 2010) with the WAG+GAMMA models. All phylogenetic trees were annotated and visualised in iTOL (Letunic, Bork, 2016).

4.2.4 Identification and classification of eukaryotic genomes

The GenBank eukaryotic genome collection was retrieved from the NCBI Genome Browser (https://www.ncbi.nlm.nih.gov/genome/browse#!/eukaryotes/), including 2,465 fungal and 4,328 protozoan genomes deposited as of as June, 2019. The reference genomes were then converted into a MinHash sketch with default k-mer and sketch sizes, using '*mash sketch*' from Mash v2.1 (Ondov *et al.*, 2016). For the MetaBAT 2 bins that were not considered 'high-quality (HQ)' by CheckM (n = 26,874), '*mash dist'* was used to estimate the distance between each query bin and its closest related reference genome (with the lowest Mash distance), and filtered by p-value < 0.05 and > 1/1000 matching-hashes. Subsequently, each MAG and its closest relative were aligned with dnadiff v.1.3 from nucmer (Kurtz *et al.*, 2004) v3.1 to compare each pair of genomes with regard to the fraction of the MAG aligned (*AlignedBases*) and ANI (*AvgIdentity*). Finally, taxonomic assignments were performed on bins that aligned with ≥ 60%

of their sequence length to the reference fungal or protozoan genomes, as previously described (Almeida *et al.*, 2019b).

4.2.5 Prediction and classification of viral sequences

Viral sequence prediction was directly performed on over 2 million metagenomic contigs longer than 5 kb (n = 2,138,702). VirFinder (Ren *et al.*, 2017) v.1.1 and VirSorter (Roux *et al.*, 2015) v1.05 were used to predict the presence of viral contigs within the 1,679 human gut assemblies generated with SPAdes and MEGAHIT. VirFinder uses a k-mer-based, machine-learning prediction model (trained on RefSeq microbial and viral sequences as of May 2015) to detect distinguishing signatures between virus and host (prokaryotic) sequences. Expected P values for the presence of viral sequences were calculated for each contig of length ≥ 5kb. Contigs are considered to contain candidate viral sequences based on the filtering criteria (score > 0.9 and p-value > 0.05) implemented in the MGnify metagenomic analysis pipeline (A. Almeida, pers. comm., July 2019). VirSorter uses a sliding-window scanning along the entire length of MAGs to call viral hallmark and viral-like genes considering viral features (i.e. similarity to known viral sequences, fraction of unknown genes, gene size spectrum, and coding strand changes frequency) derived from a manually curated reference virome database (*Viromedb*, Jan 2014). Putative viral regions within a contig are scored based on viral signal metrics, and then ranked by confidence into three categories of 'sure', 'somewhat sure' and 'not so sure' predictions. Contigs of length ≥ 5kb were considered entirely viral (phage) if the predicted viral region spans over 80% of the contig length, or otherwise prophages (i.e. viral sequences integrated in cellular genomes). Only contigs in the most confident prediction categories 1 and 4 (n = 29,693) were considered in downstream analysis. Finally, VirFinder and VirSorter predicted viral sequences were pooled and dereplicated to genetically distinct 'viral populations' (n = 21,639) based on a sequence identity threshold of 95% using CD-HIT (Fu *et al.*, n.d.) v4.8.1 (*cd-hit-est* -c 0.95).

Viral populations were then classified using the same approach for eukaryotic sequence classification. Briefly, the entire RefSeq cultured phage isolate collection (n = 9,322, as of June

2019) and the Human Gut Virome Database (GVD, *n* = 13,203, derived and predicted from 21 public gut viral metagenome and MAGs datasets as of December 2017, Gregory *et al.*, 2019) were pooled and then converted into a MinHash sketch using Mash *sketch* with default settings. Each viral population queried against the mash sketches of the viral reference database (RefSeq + GVD), and assigned the taxonomic label of its closest related viral reference genome on the basis of p-value < 0.05 and > 1/1000 matching-hashes. The host information of each viral population was either directly extracted from the GVD (predicted phyla only) or from a manually-curated database Virus-Host DB (Mihara *et al.*, 2016) for RefSeq viruses (predicted phyla and genera).

4.2.6 Prevalence rate definition

The prevalence rate was generally defined by the frequency of occurrence of MAGs or their associated taxa in relation to the entire MAG collection, rather than individual host carriage unless explicitly discussed in text. This chapter did not aim to focus on host carriage comparison as MAGs were very likely to under-estimate the carriage rate.

When taxonomic classification was performed only at the genome level, the frequency of occurrence of a given taxon is shown as the raw count of its corresponding genome bins or viral contigs across samples. When group comparisons were shown for bacterial and viral species distribution, the raw count of bacterial MAGs and taxa were normalised by groups (i.e. sampling age and delivery mode) and presented as the proportional count per group.

4.2.7 Data availability

A list of 356 eukaryotic genomic bins identified in this study is attached as Appendix 8. Due to the limit of space, the lists of prokaryotic and viral genomic bins, and data access to the MAGs are available from the Lawley Lab upon request. The customised Kraken database (HGG+pMAGs+eMAGs, *n* = 14,409) can be accessed on the Sanger public FTP site (ftp://ftp.sanger.ac.uk/pub/users/ys4/).

4.3 Results and discussion

4.3.1 Recovering over 120,000 microbial genomes from 1,679 gut metagenomes

Following a two-round metagenomic assembly process with metaSPAdes and MEGAHIT, all 1,679 metagenome assemblies produced contigs that could undergo independent binning by MetaBAT 2, MaxBin2 and CONCOCT, generating a total of 120,803 bins. For each candidate prokaryotic bin, the genome assembly quality was further evaluated with CheckM according to the level of genome completeness and contamination (Figure 4.2). By selecting the representative genome bin sets from the different variants of each bin from the original and hybridised bin sets, 13,009 non-redundant prokaryotic MAGs with more than 90% completeness and less than 5% contamination were obtained (hereafter referred to as 'high-quality', Parks *et al.*, 2017). I also generated 15,193 medium-quality MAGs with at least 50% completeness and less than 10% contamination (Bowers *et al.*, 2017), the majority of which (n = 12780, 84.1%) had a QS above 50 (defined as completeness – (5 × contamination)).

The number of genome bins across the sample age groups displayed significant variation across distinct stages (neonatal, infancy and adult) of the gut microbiota maturation (Figure 4.3a). On average, up to 100 bins were assembled from each individual adult gut metagenome (mean 55.3, 95CI% 53.0-57.6), whereas as few as 2 bins were recovered from the neonatal gut metagenomes (mean 13.6, 95%CI 13.2-13.9). This pattern is also observed with the high-quality bins, with the neonatal samples having slightly higher recovery rate than the adult samples (Figure 4.3b), largely due to the data limitations of a standard metagenomics sequencing run, which yield insufficient coverage to generate complete genomes of low-abundance organisms. Overall, these results are consistent with the observed increasing bacterial species richness (alpha diversity) over the gut microbiota developmental ages.

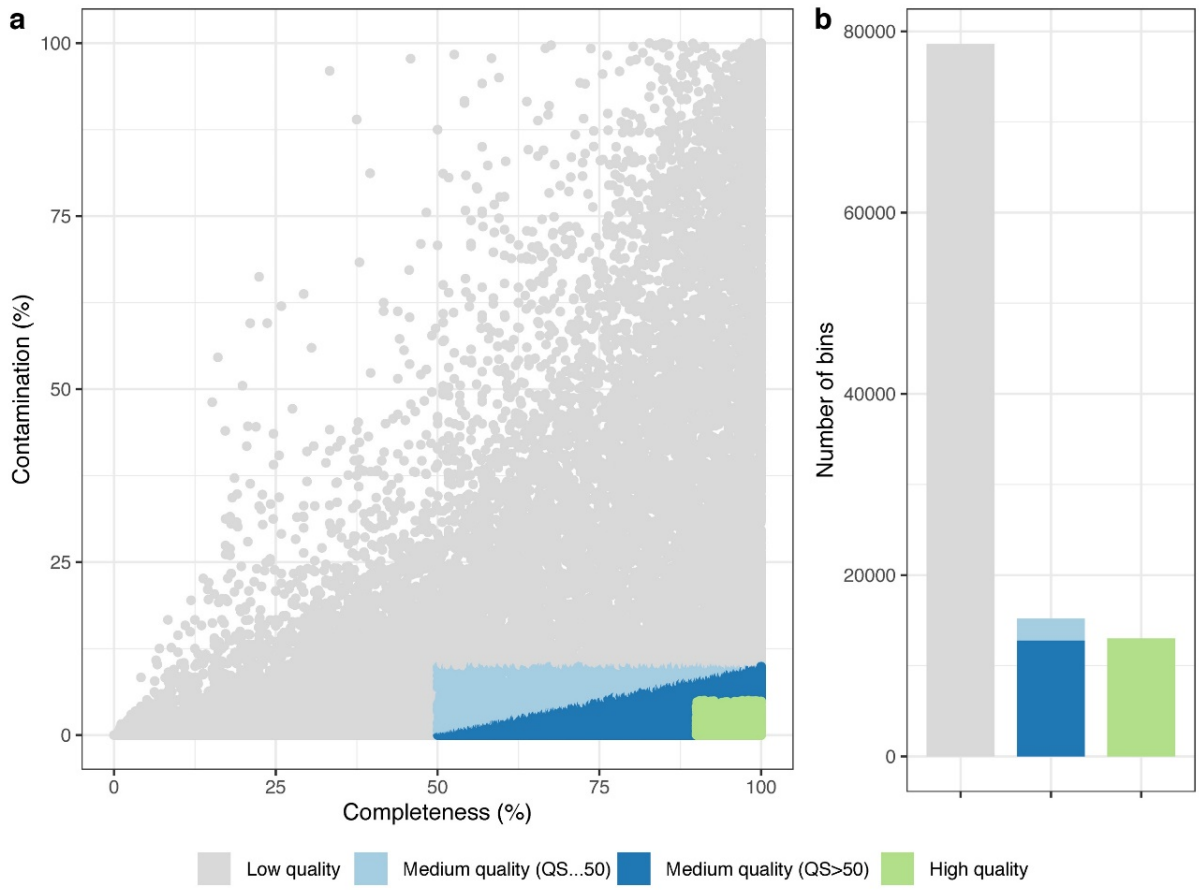

Figure 4.2 CheckM lineage workflow classification.

a, Quality metrics estimated by CheckM for the 120,803 bins generated by MetaBAT 2, MaxBin2 and CONCOCT combined. **b,** Number of bins recovered according to the level of genome completeness and contamination. QS = completeness – (5 × contamination). The high-quality bins shown are non-redundant (i.e. duplicate bins removed), whereas the low and medium quality bins originated from one or more than one binning algorithms.

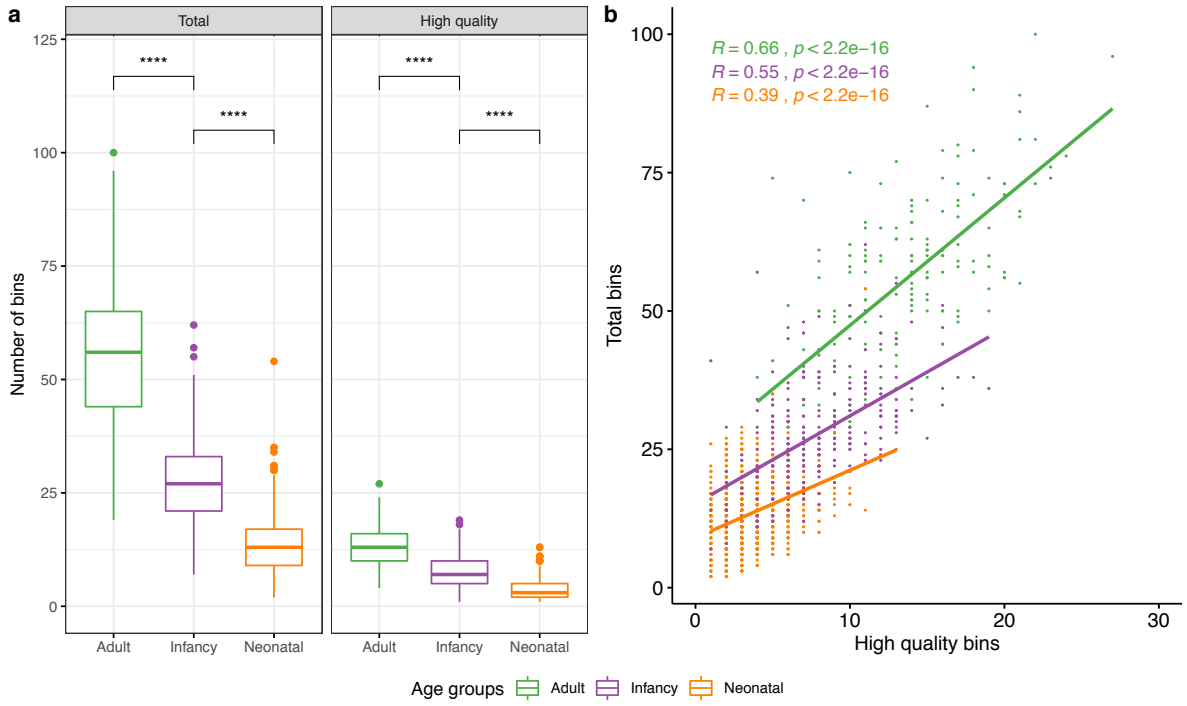

Figure 4.3 High-quality prokaryotic genome bins across age groups.

a, Boxplot showing the number of total and high-quality genomic bins assembled from gut metagenomes derived from adult (green), infancy (purple) and neonatal (orange) samples. Statistical difference between adjacent age groups was performed by two-sided Wilcoxon signed-rank test. Box lengths represent the IQR of the data, and the whiskers the lowest and highest values within 1.5 times the IQR from the first and third quartiles. **b,** Greater proportion (r=0.66) of high-quality bins were recovered in relationship to the number of total bins in adult gut metagenomes, in comparison to infant (r=0.55) and neonatal (r=0.39) samples. Count of total bins shown here is the average counts of three binning experiments. Statistical comparisons between group means were performed by two-sided Wilcoxon rank-sum tests with significance indicated (* p<0.01, ** p<0.001, *** p<0.0001, **** p<0.00001).

4.3.2 Recovery of tens of thousands of metagenomically assembled prokaryotic genomes

As CheckM exclusively relies on prokaryotic marker genes to evaluate genome quality, none of the quality-assessed MAGs would include any potential eukaryotic or viral genomes present in the gut metagenomes, that I have also investigated separately in 4.3.3 and 4.3.4. Here, I focused on characterising the high-quality, prokaryotic MAGs resolved to bacterial and archaeal lineages.

I performed taxonomic classification on 13,009 high-quality MAGs using GTDB-tk (https://github.com/Ecogenomics/GTDBTk), which provides bacterial and archaeal species assignment primarily based on whole-genome ANI distance between a query genome and its closest GTDB r89 reference genomes (23,458 bacterial and 1,248 archaeal). Consequently, 37 MAGs were classified as archaeal genomes, with the remaining large majority (n = 12,972) classified as bacterial genomes, spanning 8 phyla, 15 classes, 46 orders, 100 families, 314 genera and 651 species. All almost all bacterial MAGs could be assigned to the family level (n = 12,972) and genus levels (n = 12,942, Figure 4.4). Furthermore, 95.7% of the MAGs were assigned to the species level (n = 12,419), suggesting that the large majority of the high-quality MAGS were already represented by known bacterial genomes sequenced to date.

4.3.2.1 Taxonomy and prevalence of 651 bacterial species represented by MAGs

To place these bacterial genomes in a phylogenetic context, a maximum-likelihood phylogeny of the 12,972 MAGs was built on the basis of the 120 single-copy bacterial marker genes (Figure4.5). This analysis revealed the phylogenetic distribution of 12 most prevalent genera representing more than half of the taxonomic diversity (Figure 4.4). The majority of the most prevalent genera were known common neonatal gut microbiota colonisers, such as *Bifidobacterium* (11.3%), *Streptococcus* (7.6%), *Staphylococcus* (6.2%) and *Escherichia* (5.5%) with significantly higher prevalence rate among neonatal samples (Figure 4.6). This

observation was also in congruence with the species level classification, in which the most prevalent MAG species in the neonatal samples included *Enterococcus faecalis* (4.7%), *Staphylococcus epidermidis* (3.9%), *Bifidobacterium longum* (2.7%), *Escherichia coli* (2.6%), *Bifidobacterium bifidum* (2.1%) and *Bifidobacterium breve* (2.1%).

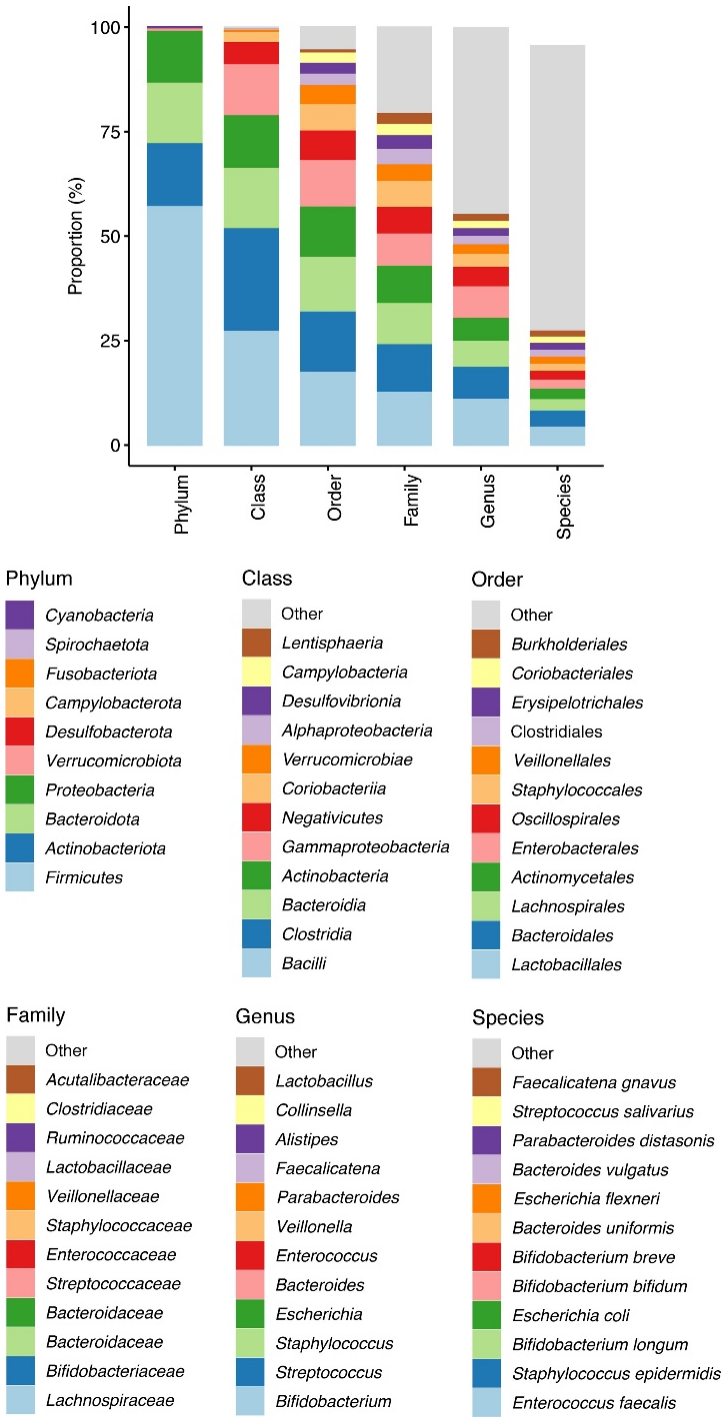

Figure 4.4 Taxonomy of the most prevalent high-quality bacterial MAGs.

Taxonomic groups ordered from top to bottom by their increasing relative proportion among 12,972 total MAGs at each taxonomic level. Only up to twelve most frequently observed taxa are shown in the legend, with the remaining lineages grouped as 'Other'.

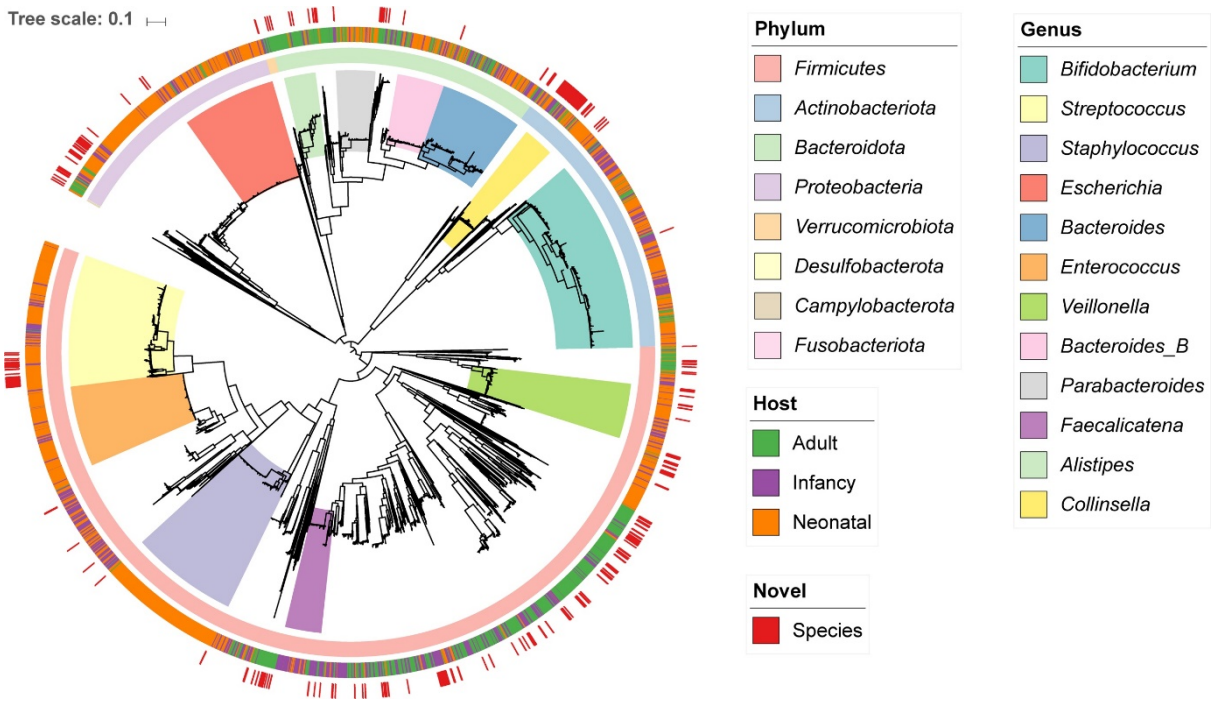

Figure 4.5 Phylogenetic tree of 12,972 high-quality bacterial MAGs.

Midpoint-rooted maximum likelihood phylogenetic tree of 12,972 high-quality bacterial MAGs based on protein alignment of the 120 bacterial single-copy genes. Twelve most prevalent genera are ranked by frequency. Inner ring: eight phyla comprising 789 species are ranked by frequency. 99.4% of the MAGs were represented by four major bacterial phyla (as per GTDB taxonomy nonmenclature) *Firmicutes* (*n* = 7,449), *Actinobacteriota* (*n* = 1,955), *Bacteroidota* (*n* = 1,875) and *Proteobacteria* (*n* = 1,611). Middle ring: the source of MAGs coloured by sample age group (adult, green; infancy, purple; neonatal, orange). Outer ring: 584 MAGs (red) considered candidate novel species (or genera and families) on the basis of topological placement on the GTDB reference genome phylogeny.

Interestingly, certain phylogenetic groups appeared to be associated with the more mature gut microbiotas in infants (e.g. *Faecalicatena [Ruminococcus] gnavus*, *Bifidobacterium infantis*) and adults (Figure 4.6), which included the genus *Alistipes* and almost the entire branch of the class *Clostridia* (i.e. family *Lachnospiraceae* and *Ruminococcaceae*), with the exception of the family *Clostridiaceae* (i.e. *C. perfringens* prevalent in neonatal samples). In particular, 84.1% (175/208 species) of the *Clostridia* species found in adult samples were absent in neonatal samples, while 40.5% (117/289 species) of the total *Clostridia* MAG species were unique in adult samples, in comparisons to just 8.3% unique neonatal *Clostridia* species. The observation that members from the class *Clostridia* are the most prevalent and diverse group in the adult gut microbiota agreed with recent findings from large public

MAGs (Almeida *et al.*, 2019b; Pasolli *et al.*, 2019) and culture collections (Forster *et al.*, 2019; Zou *et al.*, 2019) that were derived from mostly adult samples. Given that the class *Clostridia* contains the majority of the known spore-forming gut bacteria which are major contributors to inter-host transmission (Browne *et al.*, 2016; 2017), it is surprising that few spore-formers were able to colonise the neonatal gut. This points towards potential colonisation resistance and/or priority effects in early-life microbiota assembly (Sprockett *et al.*, 2018).

Previous assembly-independent metagenomic analyses have reported certain bacterial groups with differential colonisation frequency (measured by prevalence) depending on modes of delivery (Section 1.X). Here I found that the patterns of genus and species associations previously determined by read-based classification were validated in the MAG analysis, albeit using a different taxonomic classification approach and database. Specifically, members of the *Bacteroides* and *Parabacteroides* were more frequently found in babies delivered by vaginal birth, in comparison to caesarean-section-born babies (Figure 4.7). Despite having minor discrepancies in species grouping and naming due to database differences (i.e. NCBI versus GTDB taxonomy based on genome phylogeny), the MAG species associated with opportunistic pathogens including *Enterococcus faecalis*, *Clostridium perfringens* and *Klebsiella pneumoniae* (*pneumoniae*/*quasipneumoniae /variicola* in GTDB taxonomy) were also more prevalent in caesarean-section-born, neonatal samples, compared with those born vaginally (Figure 4.7). Longitudinally, the only pattern that remained statistically significant in infancy was the prevalent colonisation of *Bacteroides* and *Parabacteroides* species in vaginal-born babies, which is again consistent with my previous observation based on read classification.

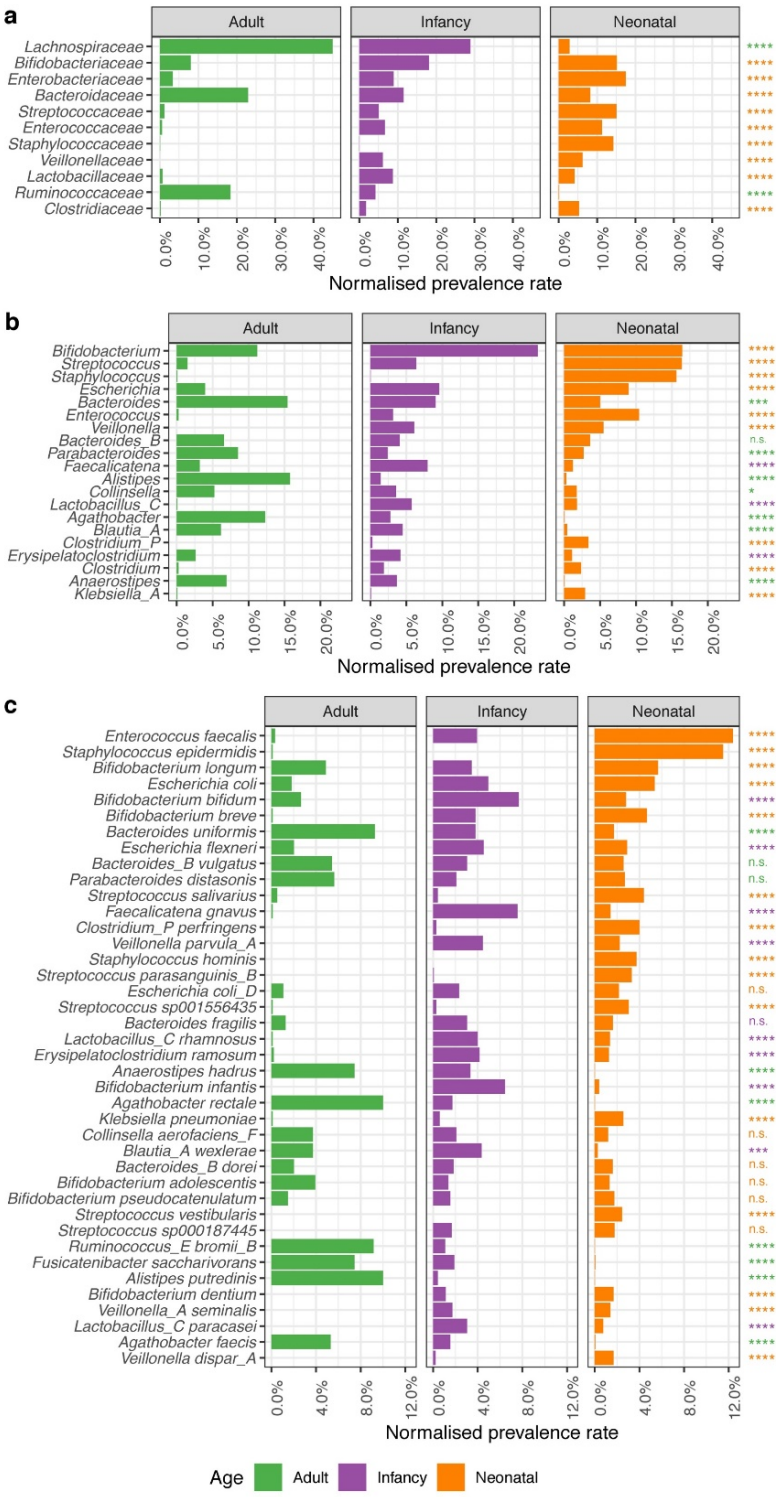

Figure 4.6 Most prevalent MAG families, genera and species across age groups.

Bar chart showing the most prevalent bacterial MAGs recovered at the family (**a**, *n* = 12), genus (**b**, n = 20) and species (**c**, *n* = 40) levels, corresponding to approximately the top 5% at each taxonomic level. The prevalence rates were normalised by the sum of total bacterial MAGs per age group (adult, green, *n* = 3,197; infancy, purple, *n* = 3,261; neonatal, orange, *n* = 6,514). Statistical significance was calculated by two-sided Fisher's exact test between groups with higher prevalence rates and coloured according to the group with significantly higher prevalence rate (n.s. P ≥ 0.05, *P < 0.05, **P < 0.01, ***P < 0.001, ****P < 0.0001).

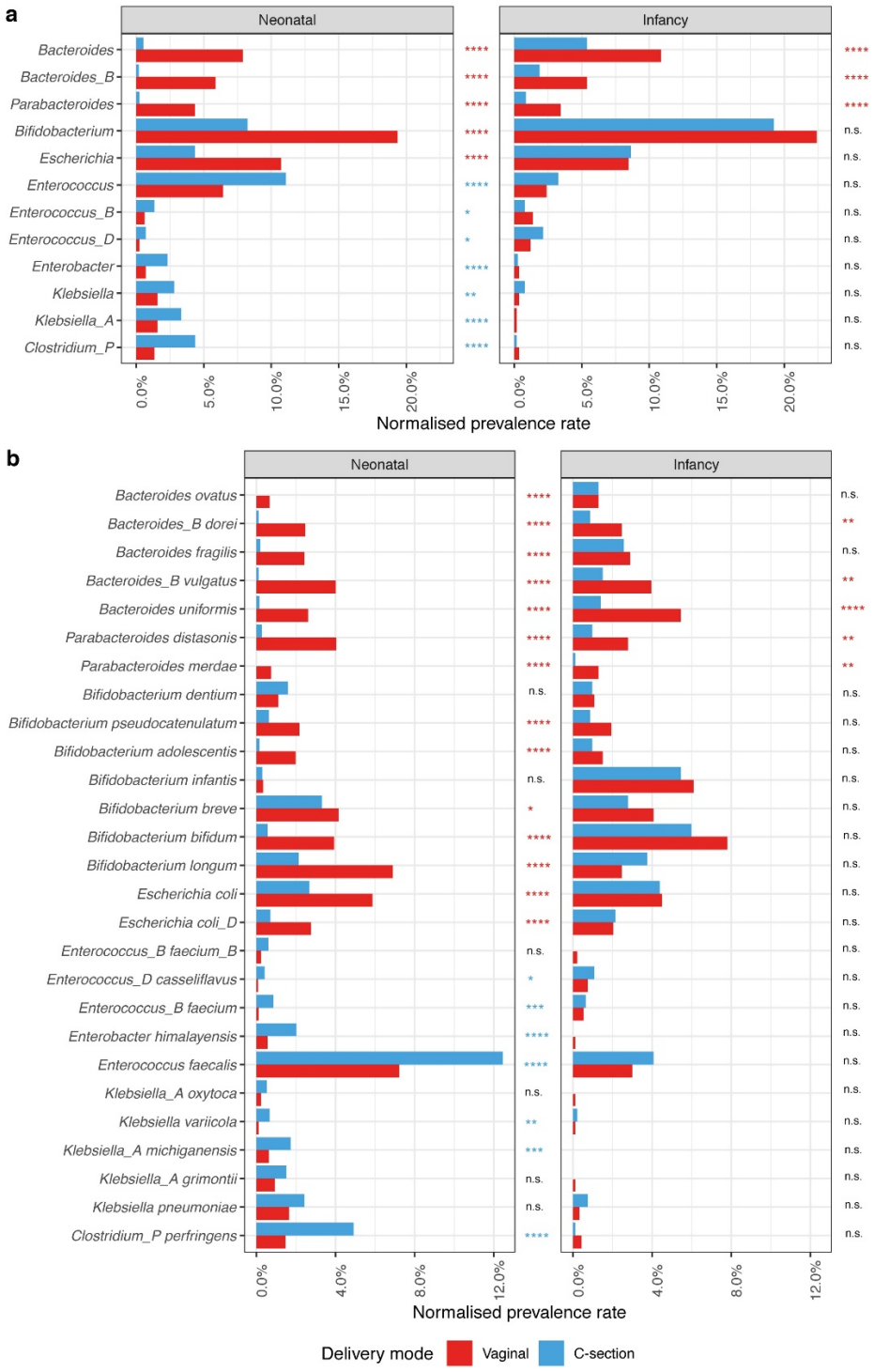

Figure 4.7 Most prevalent MAG genera and species in different modes of delivery.

Bar chart showing a selected number of bacterial genera **(a,** n = 12**),** and species (**b**, n = 27) previously associated with the mode of delivery in assembly-independent analyses. The prevalence rates were normalised by the sum of total bacterial MAGs per delivery mode group (Neonatal: vaginal, red, n = 3,370; caesarean section (C-section), blue, n = 3,144; Infancy: vaginal, n = 1,682; C-section, n = 1,555). Statistical significance was calculated by two-sided Fisher's exact test and coloured according to the group with significantly higher prevalence rate (n.s. $P \geq 0.05$, *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ****$P < 0.0001$).

4.3.2.2 Discovery of 138 uncultured bacterial taxa from hundreds of novel genomes

Of the 13,972 high-quality, bacterial MAGs, 4.2% correspond to entirely 'novel' genomes (*n* = 584) on the basis of GTDB's RefSeq 89 taxonomy as of June 2019 (Figure 4.5). In total, these 584 'novel' MAGs represented one candidate novel family (*n* = 1 MAG), 12 candidate novel genera (*n* = 30 MAGs) and 125 candidate novel species (*n* = 553 MAGs, Figure 4.8), as defined according to established genome thresholds for species delineation (≥ 95% ANI over at least 60% of the query MAG) (Varghese *et al.*, 2015; Jain *et al.*, 2018).

The uncovered 138 candidate bacterial taxa covered 7 different phyla, 11 classes, 27 orders, 59 families and 126 genera (Figure 4.8). The three most frequently assigned families were *Lachnospiraceae* (15.2%, *n* = 89), *Coriobacteriaceae* (15.1%, *n* = 88) and *Streptococcaceae* (9.3%, *n* = 54), whereas the top genera were *Collinsella* (15.1%, *n* = 88), *Streptococcus* (9.3%, *n* = 54) and *Clostridium_M* under the family *Lachnospiraceae* (6.9%, *n* = 40). Overall, 67.4% (*n* = 93) of the total candidate novel taxa were found in adult samples, 74.2% of which (*n* = 69) were absent in neonatal or infancy samples. In comparison, just 15 (10.9%) unique novel taxa were unique to the over-sampled, neonatal gut microbiotas, which did not appear to be a hotspot of uncultured bacterial diversity.

The level of prevalence and host distribution pattern of the common novel species were consistent with that of their known species counterparts. The oral and environmental associated *Haemophilus*, *Streptococcus* and *Veillonella* candidate novel species were absent in adult, but predominately found in neonatal samples (88.9%, *n* = 24; 83.3%, *n* = 45 and 84.6%, *n* =11, respectively) which were mainly from caesarean-section-born babies (75.0%, *n* = 18; 64.4%, *n* = 29 and 100%, *n* = 11). Members of the class *Clostridia*, including six major families *Lachnospiraceae*, *Clostridiaceae*, *Acutalibacteraceae*, *Ruminococcaceae*, *Oscillospiraceae*, *Peptostreptococcaceae* accounted for nearly half of the total novel taxa (48.6%, *n* = 67). In agreement with previous findings in isolate genomes, the *Clostridia* candidate novel taxa were predominately found in infancy and adult samples (81.0%, 217

out of 268 MAGs). These results suggest that despite being known colonisers of the adult gut microbiota, there is still substantial uncultured diversity within the class *Clostridia* (Almeida *et al.*, 2019b; Pasolli *et al.*, 2019; Nayfach *et al.*, 2019).

The majority of the novel taxa exhibited considerable phylogenetic diversity at the sub-family level, as indicated by the dense terminal branches and diverse ranges of ANI distances (to closest reference genomes) of the candidate novel *Lachnospiraceae* species (Figure 4.8). In contrast, certain genera such as *Collinsella* (closest to HBC strain *C. aerofaciens*), *Haemophilus* (closest to HMP strain *Haemophilus* sp. HMSC068C11) and *Streptococcus* (the branch leading up to *S. parasanguinis*) displayed very short terminal branches and ANI distance clustering (IQR 93.11-94.88%, 94.83-94.97% and 94.55-94.93%, respectively) close to the boundary of the 95% ANI threshold for species delineation, which were indicative of single-species clusters as implemented in GTDB-tk (Chaumeil *et al.*, 2019). The same phylogenetic observation regarding novel *Collinsella* species was also evident in the phylogeny of the global uncultured gut MAGs collection (Almeida *et al.*, 2019b). Indeed, recent studies have shown that C. *aerofaciens* appeared to form a species complex displaying substantial heterogeneity in metabolic capabilities (Thorasin *et al.*, 2015), while the ANI values within *C. aerofaciens* genomes ranged between 93-94% (Qin *et al.*, 2019). Furthermore, most species in the Mitis group of the genus *Streptococcus* (including the *S. parasanguinis*) have ANI values below 95% (Jensen *et al.*, 2016).

95% whole-genome ANI has emerged as a widely accepted threshold (Ciufo *et al*., 2018; Chun *et al*., 2018) for the delineation of bacterial species. This threshold is primarily supported by its strong correlation with the 70% DNA-DNA hybridization cut-off, which was considered the gold standard for circumscribing bacterial species since the 1960s (Goris *et al*., 2007). It also appears to be highly robust having be shown to recapitulate the majority of existing bacterial species (Konstantinidis, Tiedje, 2005; Jain *et al*., 2018; Olm *et al*., 2019; Parks *et al*., 2019). However, the results presented here suggest that the gold standard 95%

ANI threshold might be too high to delineate *Collinsella* and *Streptococcus* species correctly. It is thus reasonable to speculate that the novel candidate species assigned to these genera are *de facto* known bacterial species, had lower species-specific ANI thresholds been used. This potential artefact highlights the current limitation of species circumscription based on a universal ANI threshold, which warrants future genomic studies on these species with outlying ANI values, including under-studied taxa such as *Haemophilus* (15 genomes on RefSeq as of June 2019).

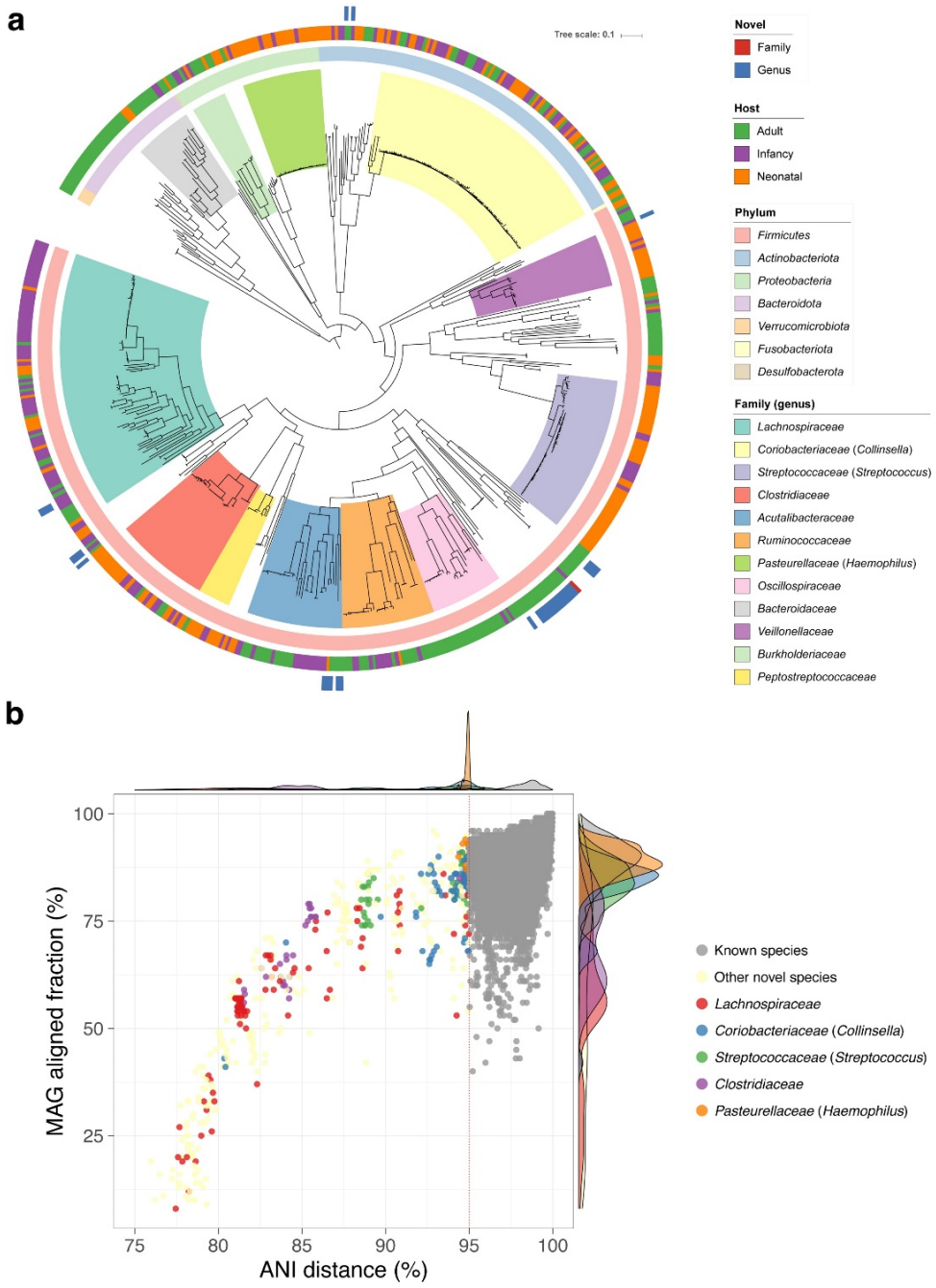

Figure 4.8 Discovery of 138 novel candidate taxa within 584 bacterial MAGs.

a, Midpoint-rooted maximum likelihood phylogenetic tree of 584 high-quality bacterial MAGs based on protein alignment of the 120 bacterial single-copy genes. Inner ring: novel candidate taxa (*n* = 138) spanning six phyla are ranked by frequency, including four major bacterial phyla *Firmicutes* (*n* = 380), *Actinobacteriota* (*n* = 109), *Proteobacteria* (*n* = 48) and *Bacteroidota* (*n* = 41). Middle ring: source of MAGs coloured by sample age group (adult, green; infancy, purple; neonatal, orange). Outer ring: candidate novel species (*n* = 125, uncoloured), genera (*n* = 12, blue) and family (*n* =1, red) determined on the basis of topological placement on the GTDB reference genome phylogeny. Twelve most prevalent families are ranked by the frequency with the predominant genus reported in brackets if applicable. **b,** Candidate novel species (coloured by a selected number of most prevalent families) was assigned based on its phylogenetic placement and aligned less than 95% ANI (red, dotted line representing the gold standard species circumscription threshold) with its closest reference genome in the GTDB phylogeny.

4.3.2.3 Limited archaeal diversity and rare presence

Of the 37 of 13,009 (0.28%) high-quality prokaryotic MAGs assigned to the archaeal domain, all were classified as methanogenic archaea belonging to 3 species under the family *Methanobacteriaceae* (Figure 4.9). All but one MAG (*Methanosphaera stadtmanae*) belonged to two species closely related to *Methanobrevibacter smithii,* which agreed with the dominant presence of gut methanogens observed in a recent large-scale metagenomic assembly study (Pasolli *et al.*, 2019). Archaeal MAGs were only found in adults and were absent in infancy and neonatal samples. These results agreed with the observations in previous birth cohorts (Bäckhed et al., 2015), suggesting that archaeal colonisation in very early life is much rarer than in adults.

Given that both archaeal species detected here were previously considered ubiquitous colonisers of the gut microbiota with up to 95.7% prevalence in adults according to dna-based detection (Dridi *et al.*, 2009), both the overall prevalence of archaea in relation to the total MAG count (0.28%) and host carriage (4.8%, 37 out of 771 subjects) in this study seemed surprisingly low. Nevertheless, the archaeal MAGs prevalence reported in this study was in fact within the range (0.10-0.96%) reported in two recent large-scale metagenomic assembly studies (39/40030, Almeida *et al.*, 2019b; 675/70178, Pasolli *et al.*, 2019). Whilst no archaeal genome was present in the HGG database used in this study, inclusion of the archaeal MAGs recovered herein in Kraken taxonomic classification returned an estimation of 7.8% for the host carriage rate (60 gut metagenomes/individuals), which was similar to the 6.5% prevalence in the HMP1-II gut metagenomes (Lloyd-Price *et al.*, 2017).

Taken together, these results suggest that any potential bias that might have led to under-estimation of archaea was unlikely attributed to the assembly approach itself. Rather, the bacteria-targeting DNA extraction protocols used in most gut metagenomic studies (including the BBS) were most likely not effective for extracting archaeal DNA, which seemed to require double mechanical lysis for breaking proteinase K-resistant cell wall (Dridi *et al.*, 2009).

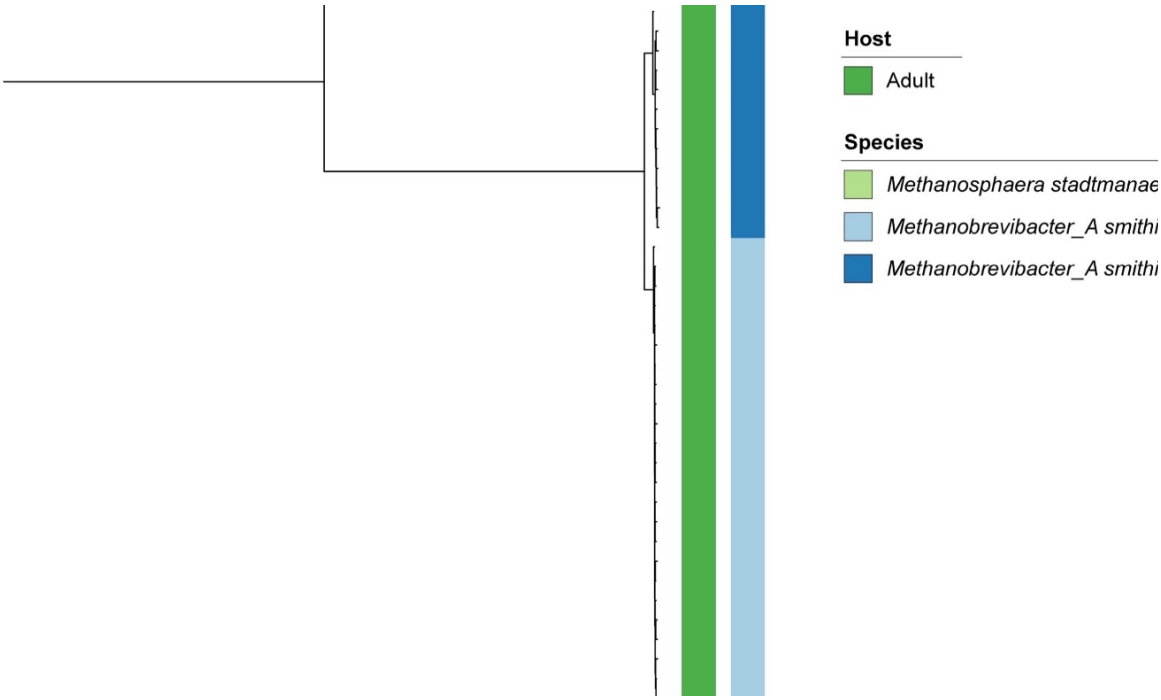

Figure 4.9 Phylogenetic tree of 37 high-quality archaeal MAGs.

Midpoint-rooted maximum likelihood phylogenetic tree of 37 high-quality archaeal MAGs based on protein alignment of the 122 archaeal single-copy genes. All MAGs originated from adult (green) samples. A total of 3 recovered methanogenic archaeal species belonging to the family *Methanobacteriaceae* shown were ranked by ascending frequency.

4.3.2.4 Prokaryotic MAGs substantially expanded the unexplored species repertoire

Having identified 792 species (789 bacterial and three archaeal species) represented by 13,009 prokaryotic MAGs, I then investigated what proportion of the BBS MAGs collection overlapped with 530 cultured species represented by isolate genomes in the HGG database. Briefly, I attempted to assign each MAG to its closest HGG genome as measured by Mash distance, and then performed a pairwise comparison to determine if they were identical species using an established criterion of ≥60% of the MAG aligned with ≥95% ANI. Of the 13,009 prokaryotic MAGs, 73.8% (n = 9,598) assigned to 279 HGG species, 44.4% of which had ≥99% ANI indicating closely related strains (Figure 4.10a). In addition, 40 novel MAGs corresponding to 8 out of 138 novel species were found in the HGG collection. Overall, this MAG collection represented a substantial expansion of the unexplored prokaryotic diversity (63.8%, 505/792 non-HGG species) in the BBS gut metagenomes.

Of the 3411 unassigned MAGs, the families *Streptococcaceae*, *Staphylococcaceae* and *Veillonellaceae* included more frequently detected genomes (prevalence 0.7-1.3%, Figure 4.10b-c) as these were all known colonisers of the neonatal gut microbiota, representing 27.4% of total unassigned MAGs (n = 936). However, this was not reflected in their reduced within-clade diversity (unassigned MAGs/species ratio: 14.4, 43.6 and 20.8, respectively), in comparison to the families *Lachnospiraceae*, *Enterobacteriaceae*, *Oscillospiraceae* (unassigned MAGs/species ratio: 3.8, 3.2 and 4.2, respectively) for which MAGs substantially expanded the species diversity missing in the HGG. Importantly, 88.1% (445/505) of the expanded the non-HGG species repertoire were rare species with <0.1% prevalence, a proportion significantly higher than that in the HGG-matched species (58.8%, 164/279; $p<0.0001$, two-sided Fisher's exact test). These results indicated that most of the expanded phylogenetic diversity in the prokaryotic MAGs resided in non-core taxa, which could greatly complement the HGG database.

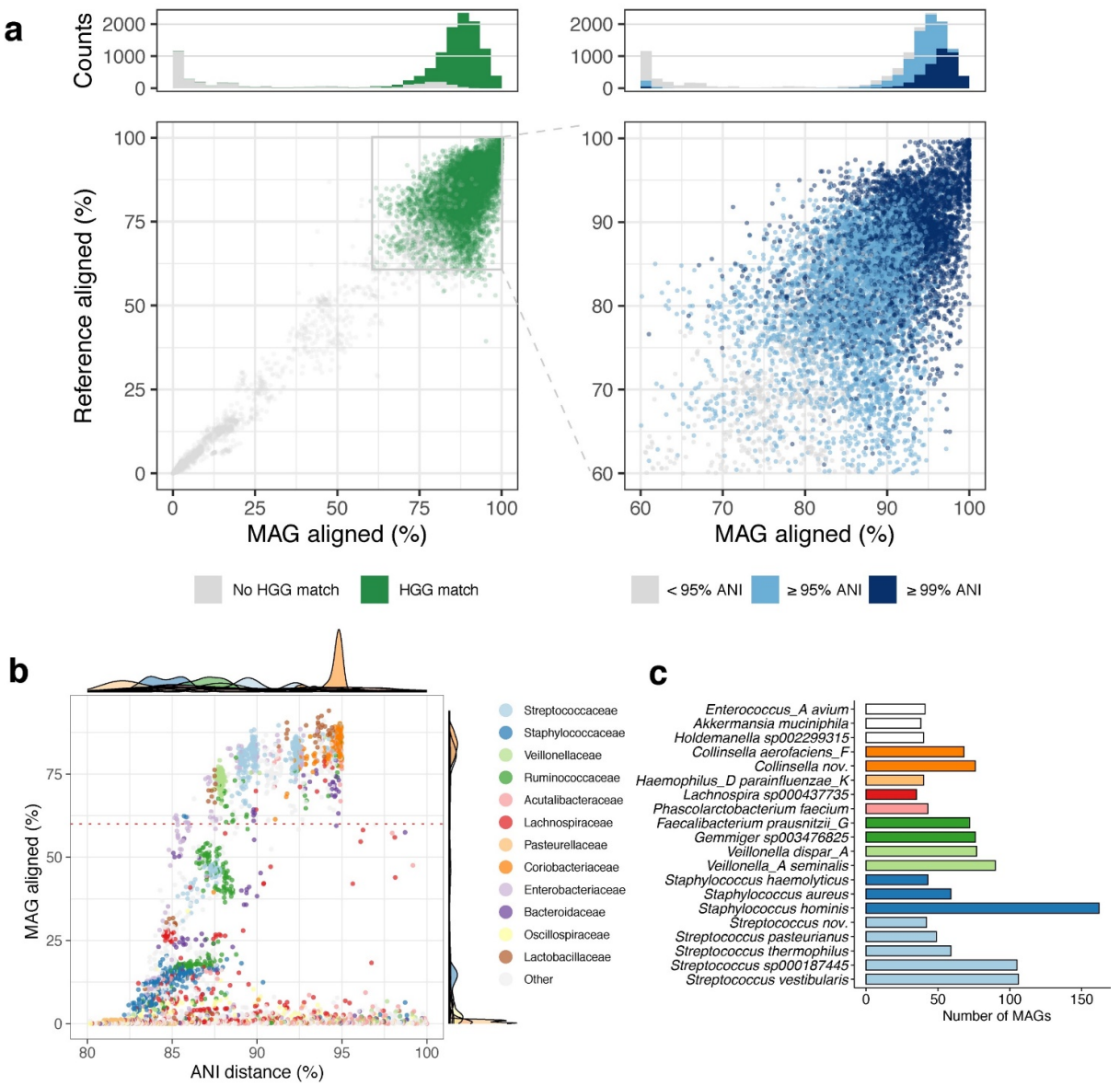

Figure 4.10 Thousands of MAGs expanded the untapped prokaryotic diversity.

a, Left, high-quality (>90% completeness, <5% contamination) prokaryotic MAGs that matched the HGG genome (green; ≥95% average nucleotide identity over at least 60% of the genome) and those that could not be classified (grey). Right, expanded view of MAGs with an alignment fraction of at least 60%, coloured on the basis of the ANI in relation to the best matching HGG genome. **b,** MAGs that could not be assigned to the HGG database (n = 3,411) across 12 most common families (coloured) ranked in descending order. Phylogenetic diversity within a given family could be estimated by the ANI value distribution of its MAGs, as evident by the peaks in the density plot displayed on top (e.g. low diversity in *Coriobacteriaceae*, *Streptoccaceae*, *Veillonellaceae* and *Pasteurellaceae*). As previously observed in novel candidate *Collinsella* species, the *Collinsella* (*Coriobacteriaceae*) MAGs (n = 155) displayed herein grouped into a tight ANI cluster close to the 95% ANI species delineation cut-off (IQR = 94.07-94.88%), indicating that these MAGs likely belonged to their closest HGG species. **c,** Frequency of occurrence of 20 most common MAG species (coloured by family) not represented in the HGG database.

4.3.3 Composition and prevalence of microbial eukaryotes

Whilst in this chapter I have primarily focused on the diversity of prokaryotic organisms present in the recovered MAGs, I also investigated how many of the BBS genome bins represented known non-prokaryotic organisms, including eukaryotic and viral sequences. In this section, I present the results of the genome bins that were predicted to belong to microbial eukaryotes (microeukaryotes).

To identify potential eukaryotic organisms, I expanded the search pool to the entire MAG collection apart from those that CheckM had confidently predicted to be prokaryotic or 'high-quality (HQ)'. To avoid counting duplicate bins, a total of 26,874 non-HQ, MetaBAT 2 genome bins were searched against the entire GenBank collection of fungal and protozoan genomes (*n* = 6,793). Consequently, 356 eukaryotic genome bins had at least 60% of their genome aligned to a known eukaryotic organism (46 unique genome isolates), representing a total of 18 fungal and two protozoan species (Figure 4.11, Appendix 8).

4.3.3.1 Protozoa

Both protozoal species identified in the BBS dataset, *Blastocystis sp.* (*n* = 14 genomes; three subtypes ST1, ST4 and ST6 of 1, 1 and 12 genomes, respectively) and *Cyclospora cayetanensis* (*n* = 268 genomes) are among the most common eukaryotes found in the human gut microbiota as reported in recent large-scale human gut metagenomic assembly studies (Almeida *et al.*, 2019b; Pasolli *et al.*, 2019). Among them, *Blastocystis* is an intestinal eukaryotic parasite best known for its high prevalence of commensal carriage in the human gut microbiota, with colonisation rate ranging from 0.5 to 30% of humans in industrialised societies (Scanlan *et al.*, 2014; Krogsgaard *et al.*, 2015; Beghini *et al.*, 2017; Tito *et al.*, 2019), and up to 100% in non-industrialised countries (Safadi *et al.*, 2014; Ramírez *et al.*, 2017; Nieves-Ramírez *et al.*, 2018).

In the healthy UK adults and infants sampled in this cohort, the prevalence of *Blastocystis* is only 1.68% (13 out of 771 individuals) with a higher rate of carriage observed in adults than in

infants (4.0% versus 1.0%, p = 0.0136, two-sided Fisher's exact test). The infrequent *Blastocytis* carriage in the UK infant gut microbiota reported here is in agreement with its very low prevalence (0-5%) previously observed in infants from Europe (Wampach *et al.*, 2017; Scanlan *et al.*, 2018), United States (Scanlan *et al.*, 2016) and India (Pandey *et al.*, 2012; 2015), indicating that the developing early-life microbiota might not provide the conditions (e.g. ecological niche or microbial interactions) needed for successful *Blastocytis* colonisation.

It is worth noting that *Blastocystis* prevalence rates can vary significantly by geographical regions, as the adult carriage (4%) in this UK cohort is also substantially lower than the 30-65% prevalence rates observed in Irish (Scanlan *et al.*, 2014), Mexican (Nieves-Ramírez *et al.*, 2018), Cameroonian (Lokmer *et al.*, 2019) and Belgian (Tito *et al.*, 2019) adults, and in children from Colombia (Ramírez *et al.*, 2017), Nigeria (Poulsen *et al.*, 2016) and Senegal (Safadi *et al.*, 2014). Therefore, the variation in prevalence rates could potentially result from differential *Blastocytis* related to living and sanitation conditions (e.g. exposure to contaminated water). Differences in the prevalence of *Blastocytis* could also be attributed to methodological variations, including the methods of DNA extraction and *in silico* detection (Beghini *et al.*, 2017). In fact, the DNA extraction protocol deployed in this study was not designed for breaking down lysis-resistant micro-eukaryotes that require extra mechanical lysis steps (Yoshikawa *et al.*, 2011), whilst *Blastocytis* detection relied on sequence mapping using relatively conservative detection criteria. Compared with the PCR and 18S rRNA amplicon sequencing methods used in all previous studies, mapping much longer MAG sequences (IQR = 207.4-312.3 kbp) is deemed to be less sensitive (recall) but more precise (true positive recovery). Indeed, the rate of *Blastocytis* recovery (1.69% versus 1.01%, p = 0.097, two-sided Fisher's exact test) from the BBS MAGs, as well as the relatively poor MAGs alignment coverage (Figure 4.11b, 1.04% versus 0.97%, two-sided Wilcoxon signed-rank test) were at the same levels as reported in recent large-scale, human gut metagenomic assembly studies (Almeida *et al.*, 2019b; Pasolli *et al.*, 2019).

The other identified protozoan species, *Cyclospora cayetanensis,* is a relatively overlooked enteric parasite known as an opportunistic pathogen responsible for human cyclosporiasis, an emerging worldwide cause of diarrhoea (Ortega, Sanchez, 2010). This species had recently been reported as the most common microeukaryotes in the adult gut MAG datasets (Almeida *et al.*, 2019b) with a global prevalence rate of 3.6% (431 out of 11850 samples). This finding is indeed validated in the BBS dataset (Figure 4.11a), which has an even higher prevalence rate of 22.9% (n = 176 out of 771 subjects). *Cyclospora cayetanensis* was more frequently carried by adults as detected in the majority of the BBS mothers (64.6%; n = 113 out of 175 subjects), in comparison around 10% of the BBS babies (n = 62 out of 596 subjects, $p < 0.0001$, two-sided Fisher's exact test). Whilst its prevalence rate is previously known to vary between 0% to 41.6% (Peru, Chacín-Bonilla, 2010), the observed prevalence in the UK infants is at least comparable, if not higher than previous reports in children from tropical and sub-tropical endemic regions, including Peru (10.9%, Ortega *et al.*, 1993), Thailand (2.2%, Thima *et al.*, 2014) and Nepal (10.1%, Bhandari *et al.*, 2015), suggesting that *Cyclospora cayetanensis* could be an underappreciated, common coloniser of the human microbiota in early life. Given that most of the infected cases were asymptomatic (Chacín-Bonilla, 2010), it might not be surprising to identify this intestinal parasite in the healthy carrier gut metagenomes.

Interestingly, all the MAGs identified as *Cyclospora cayetanensis* in this study were mapped to only one reference genome (GCA_002893375.1), which appears to differ substantially in genome size (37.4 Mb) and GC% content than the other 36 *Cyclospora cayetanensis* public genomes on the GenBank (representative genome GCA_002999335.1, 44.3 Mb, 51.90% GC). Closer inspection of this genome identified several contigs with >99% alignment with bacterial genomes belong to different phyla (*Akkermansia* sp., GCF_004167605.1; *Bacteroides uniformis*; GCF_003468755.1; *Faecalibacterium prausnitzii*; GCF_003287405), suggesting that this *Cyclospora cayetanensis* genome was likely severely contaminated. Future studies

should implement new tools to carefully assess the quality of eukaryotic MAGs and public reference genomes (Waterhouse *et al.*, 2018; Saary *et al.*, 2019).

In summary, by performing the first metagenomic screening of protozoan species in the neonatal gut microbiota, I identified two common, asymptomatically-carried protozoan colonisers in this large UK cohort. While the main study result agrees with previous 'eukaryome' studies reporting that early colonisation of *Blastocysis* is rare, this observation will need to be validated in other large cohorts from geographically diverse regions, as very few studies to date attempted gut protozoa detection using a state-of-the-art metagenomics (assembly or mapping) approach. Carriage of the intestinal parasite such as *Blastocystis* sp. had previously been associated with changes in the richness and diversity of the gut bacteria (Audebert *et al.*, 2016; Beghini *et al.*, 2017; Partida-Rodriguez *et al.*, 2019). Whilst the within-sample protozoa-bacteria interaction was not assessed in this study due to insufficient sampling of *Blastocystis*, future studies should further investigate its potentially critical ecological role in the gut microbiota community (Laforest-Lapointe, Arrieta, 2018).

4.3.3.2 Fungi

Of the 18 fungal species represented by 74 genome bins, 12 were found in 47 neonates (60.9% caesarean-section-born, 7.9% carriage rate) and nine species in 11 infants (36.4% caesarean-section-born, 3.6% carriage rate), but none in adults (Figure 4.11a). The lack of 'mycobiome' detected in adult MAGs might come as a surprise, given that fungi were claimed to be ubiquitous in HMP samples (Nash *et al.*, 2017) in one of the few large-scale gut 'mycobiome' studies to date. However, in a follow-up study, the same group of authors rejected this claim by concluding that fungi detected in stool samples were only transiently present from the diet or oral cavity, and therefore there was no fungal colonisation in the 'healthy' human gut microbiota (Auchtung *et al.*, 2018). In addition, the lack of human gut 'mycobiome' was supported by the recent large-scale gut metagenomic assembly studies in which fungi were found in only 0.02% of the individuals (Almeida *et al.*, 2019b; Pasolli *et al.*, 2019). The fungal

carriage in BBS neonates and infants reported herein (3.6-7.9%) were comparable with the other metagenome assembly-based study in premature infants (6%, Olm *et al.*, 2019) also substantially lower than previous estimations based on culturing (23-80%, Strati *et al.*, 2016; Suhr, Hallen-Adams, 2017) and qPCR of the fungal Internal Transcribed Spacer (ITS) region (37% - 76%, Wampach *et al.*, 2017; Schei *et al.*, 2017). Other than the variation in DNA extraction protocols, these differences might also be attributed to the much more complete fungal ITS databases (e.g. >1,000,000 references on UNITE (https://unite.ut.ee/)). Nevertheless, shotgun-sequencing approach might not be sensitive to identify fungal sequences that were usually present at extremely low DNA level in stool samples (i.e. 0.001-0.01%, Nash *et al.*, 2017; Auchtung *et al.*, 2018), whilst read-mapping detection of fungal DNA had an estimated limit of detection of 0.05% relative abundance (Olm *et al.*, 2019).

All the common fungal species detected in the BBS MAGs, namely the *Candida* species (C. *albicans, C. parapsilosis* and *C. tropicalis*) and *Saccharomyces cerevisiae* concurred with previous findings (Fujimura *et al.*, 2016; Wampach *et al.*, 2017; Ward *et al.*, 2018). In particular, *Candida* and *Saccharomyces* species were recently reported to be most frequently transmitted from the hospital room to newborn babies (Olm *et al.*, 2019; Heisel *et al.*, 2019). Furthermore, I also detected opportunistic fungal pathogens such as *Clavispora lusitaniae*, *Geotrichum candidum*, *Rhodotorula mucilaginosa*, *Pichia kudriavzevii*, *Mucor racemosus*, *Lodderomyces elongisporus*, as well fungi associated with dairy products and breast milk (Boix-Amorós *et al.*, 2019) including *Penicillium spp*., *Kluyveromyces marxianus, Naumovozyma dairenensis*.

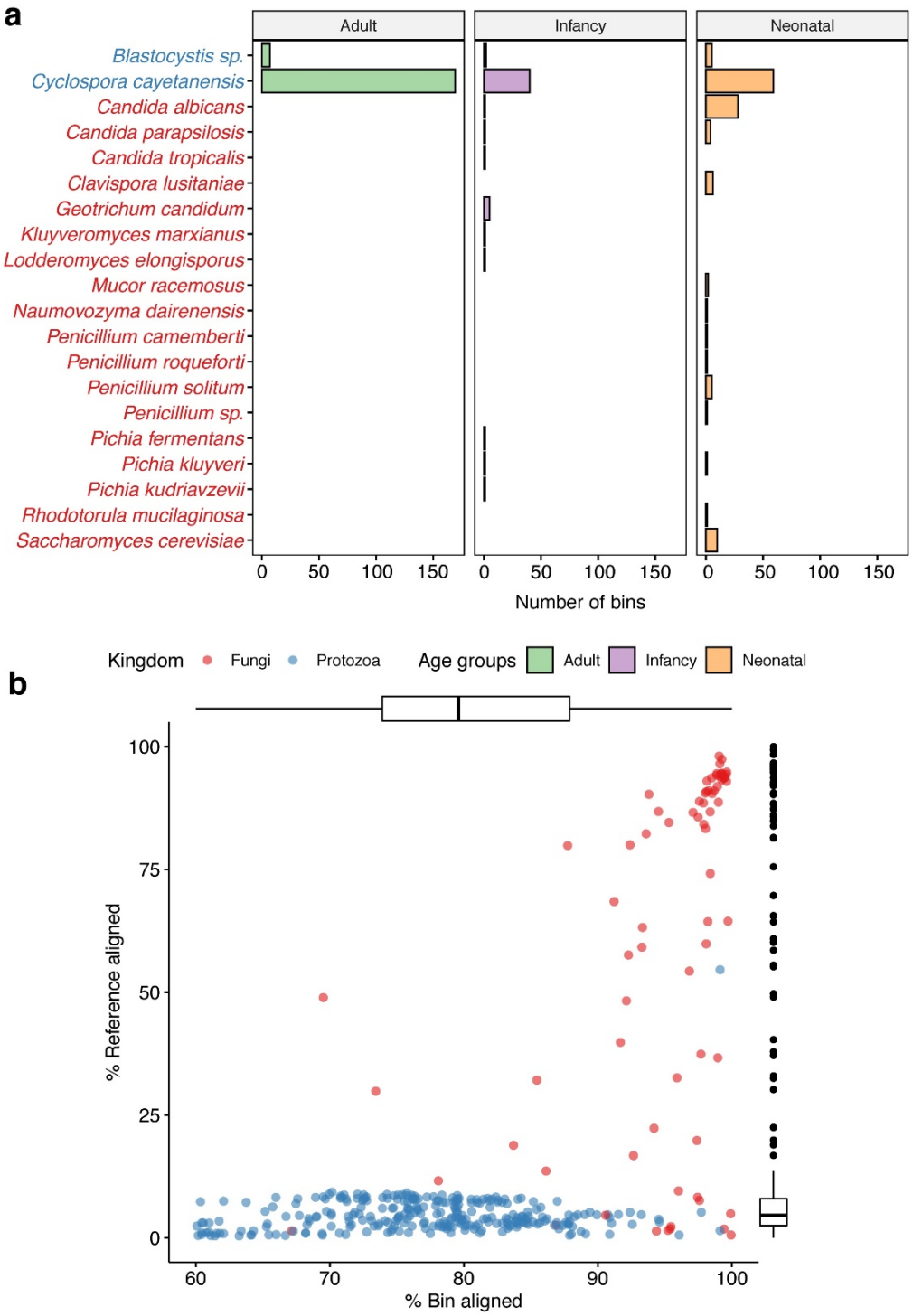

Figure 4.11 Composition and prevalence of the microbial eukaryotic MAGs.

a, Bar chart showing age group distribution of the 356 eukaryotic genome bins that matched to RefSeq eukaryotic genomes with ≥60% query alignment faction (IQR = 73.9-87.9%). **b,** Majority of the fungal genomes (red, *n* = 74) could be assembled from a single bin with higher genome completeness (IQR = 21.7-92.1%), in contrast to the highly incomplete (IQR = 2.5-7.2%) protozoan genomes (blue, *n* = 282) that mapped relatively poorly to the reference genomes. Statistical difference in mean reference proportion aligned (60.3% versus 4.7%, p<0.0001), and mean bin proportion aligned (95.0% versus 77.3%, p<0.0001) between fungal and protozoan genomes was determined by two-sided Wilcoxon signed-rank test. Box lengths represent the IQR of the data, and the whiskers the lowest and highest values within 1.5 times the IQR from the first and third quartiles.

4.3.4 Uncovering viral dark matter

The putative viral sequences present in the gut metagenomes could include viruses and proviruses (integrated into host genomes) that infect both prokaryotic (phages and prophages) and eukaryotic hosts. Given that most viral sequences are embedded in prokaryotic or eukaryotic metagenomes and therefore were rarely found to be binned together (Hurwitz *et al.*, 2018), viral predictions were directly performed on the metagenome assemblies prior to the binning step using state-of-the-art viral sequence prediction tools VirFinder and VirSorter.

To increase the sensitivity of free virus (i.e. double-stranded DNA) detection, this study exclusively considered contigs with a minimum of 5 kb in length. A total of over 2 million metagenomic contigs assembled from 1,679 samples were screened for viral sequence features based on highly conservative criteria (Methods), resulting in the identification of 29,693 putative DNA metagenomic viral contigs (Figure 4.12a). The assembled viral contigs further clustered into 21,639 genetically distinct 'viral populations' based on 95% nucleotide sequence identity (Bobay, Ochman, 2018; Roux *et al.*, 2019), indicating substantial virome diversity within the gut metagenomes. To my knowledge, both the numbers of assembled viral contigs and viral populations represent the single largest gut virome discovery to date.

Most of the neonatal samples (90.4%) were detected with at least one viral sequence (IQR = 2-5), based on the most conservative estimation (VirSorter, Figure 4.12b), confirming previous reports of early colonisation of viral populations shortly after birth(Lim *et al.*, 2015; Reyes *et al.*, 2015). Similar to the observation of increasing load of bacterial MAGs over developmental age, the gut virome richness was projected to increase over the microbiota maturation trajectory through stages of infancy (IQR = 4-10 viral sequences) and adult (IQR = 36-66 viral sequences) based on the upper boundary estimation (VirFinder, Figure 4.12b).

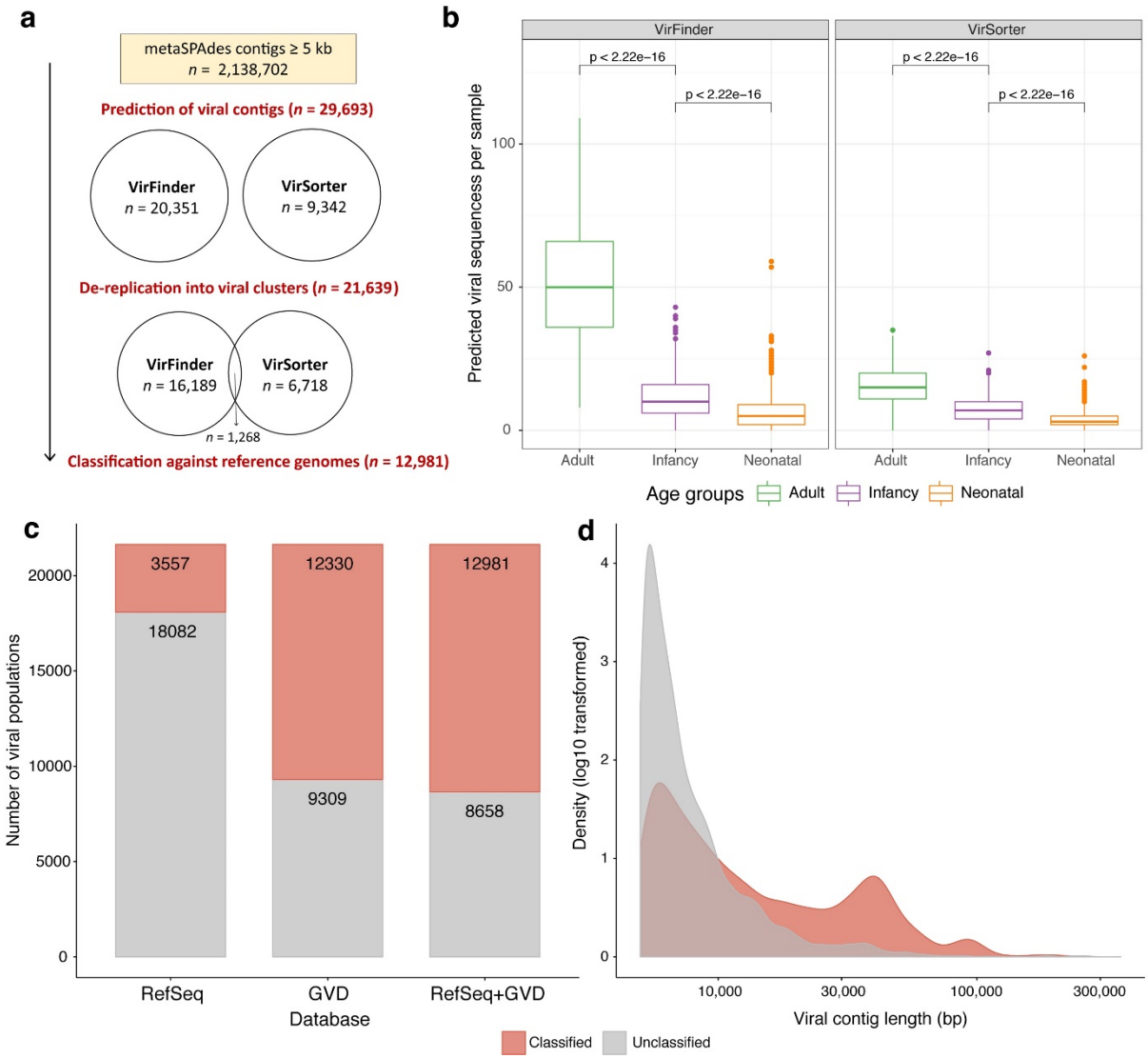

Figure 4.12 Thousands of novel gut viral populations recovered from assemblies

a, Schematic diagram showing the methodological steps of viral sequence prediction and corresponding statistics. **b,** Boxplots showing the number of viral sequences predicted by two software (VirFinder, VirSorter) used in this study. Boxplots lower and upper hinges correspond to the first and third quartiles (the 25th and 75th percentiles), while whiskers extend from the nearest hinge to the smallest/largest value no further than 1.5 * IQR from the hinge (where IQR is the inter-quartile range, or distance between the first and third quartiles). **c,** Number of de-replicated and classified viral populations after mapping to known viral sequences in the RefSeq and the Gut Virome Database (GVD) and their size distribution (**d**).

4.3.4.1 Composition and prevalence of the neonatal gut viruses.

Of the 21,639 viral populations clustered at 95% sequence identity, only 16.4% matched to cultured phage isolates in the RefSeq viral database (n = 3557) and 60% when also considering uncultured, gut viral MAGs sequences in the GVD (n = 12,981, Figure 4.12c). In particular, 78.9% of the long viral contigs (≥10kb in length) could be assigned to a known viral sequence, in contrast to 47.5% of the short viral contigs <10kb (Figure 4.12d). Taxonomically, the 12,981 classified viral populations and 18,517 contigs were represented by a total of 3,336 viral species (3178 GVD viruses and 157 RefSeq cultured phages), of which 99.8% were bacterial viruses (bacteriophages), and tiny proportion of eukaryotic (0.18%) and archaeal (0.02%) viruses (Figure 4.13a). Among the bacteriophages, 55.8% did not have a taxonomic classification in the curated RefSeq phages or novel viruses predicted by the GVD, with the remaining fraction comprised of the expansive *Caudovirales* order of dsDNA phage families (*Siphoviridae*, *Myoviridae* and *Podoviridae*) and the ssDNA virulent phage family *Microviridae*. In addition, none of the four archaeal viral populations matched to any of the known archaeal viruses. These results highlighted a significant taxonomic classification gap for gut phage and archaeal virus (Shkoporov, Hill, 2019), which were still largely underrepresented and uncharacterised in public databases with unresolved and/or missing taxonomic assignments, despite recent substantial expansions of the reference viral genomes (Paez-Espino *et al.*, 2016; 2017; Gregory *et al.*, 2019).

Of those viral populations that could be classified to known viral species, I sought to investigate their prevalence in the BBS samples, and establish if any ubiquitous viral species (detected in all samples) that could define a 'core' gut virome (Manrique *et al.*, 2016). On average, 9.36±10.83 (mean ± SD; range: 0 to 69) unique viral species were detected per sample, but no viral species were found across all samples. Using an extremely relaxed threshold to represent the 'core' gut virome in the BBS samples, only 14 viral species (0.42% of total species) were present in more than 5% of the study samples. Most viral species were detected in very few

samples. In fact, 86.6% of the species were found in <0.5% of the samples and 45.0% of the species were unique to a single sample. This pattern seemed to be associated with the degree of 'bacteriome' heterogeneity as 17 species (1.95% of neonatal species) were shared by 5% of the neonatal samples, in contrast to 110 'core' viral species in the adult samples (5.0% of total adult species). Specifically, the adult gut virome exhibited higher complexity (~2.5 times more unique species than neonatal), whereas the neonatal gut virome displayed a high degree of inter-sample/individual variability evident by the lack of dominant viral species (Figure 4.13b). These results highlighted the dynamic and personal-specific nature of the early-life gut virome, and also supported the recent claims regarding the lack of 'core' human gut virome (Minot et al., 2011; Carding *et al.*, 2017; Shkoporov *et al.*, 2019a; Gregory *et al.*, 2019).

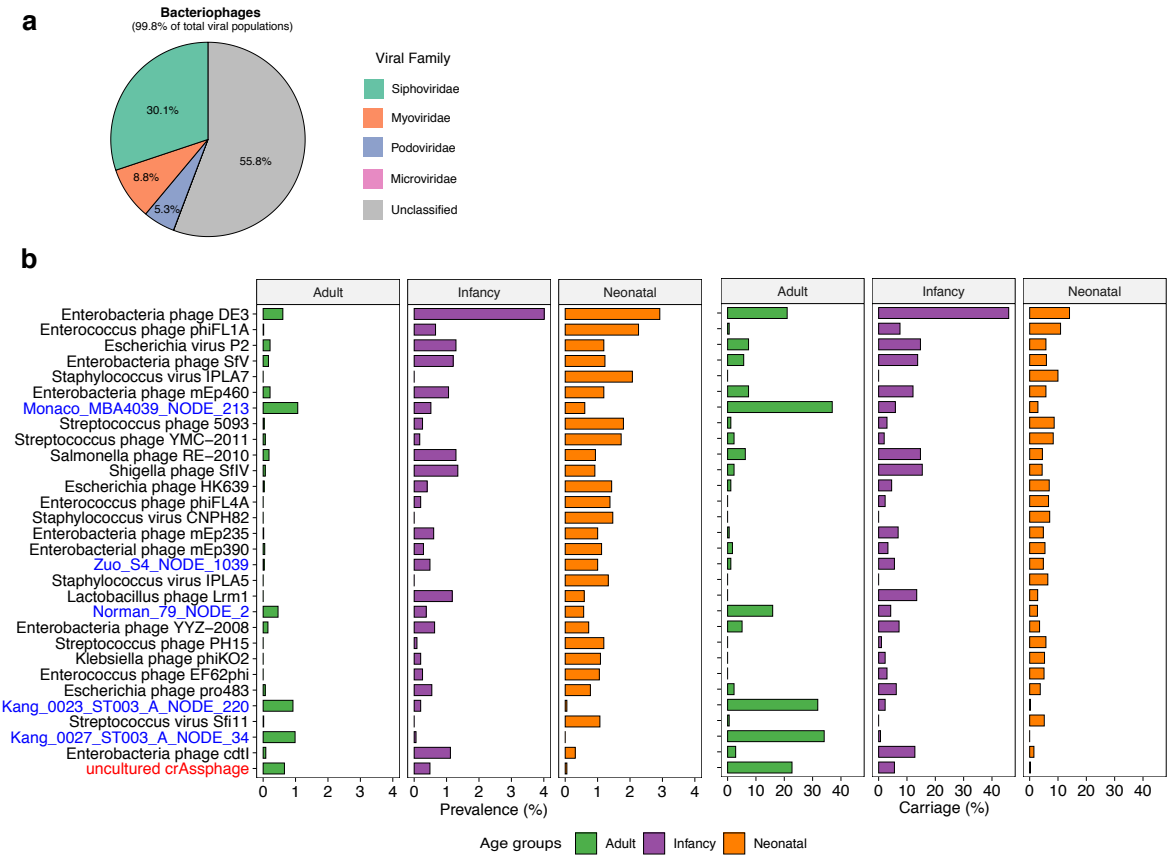

Figure 4.13 Composition and prevalence of the gut viruses

a, A Pie chart showing the proportion of major families in the BBS bacteriophages (viral populations). **b,** Bar chart showing the prevalence (left, normalised by contig count per group) and carriage rate (right, normalised by sample size per group) of the top 1% viral species (*n* = 30) contigs across sample age groups. Uncultured viral species represented by MAGs with unresolved taxonomy were coloured in blue, with crAssphage coloured in red.

4.3.4.2 The neonatal gut virome is shaped by phage-infected bacterial colonisers

CrAssphages were well-known to be widespread in the human gut virome (Dutilh *et al.*, 2014; Guerin *et al.*, 2018; Edwards *et al.*, 2019). Whilst as many as eight different crAssphage populations were detected in the study samples, they were not the most common phage in the adult gut viromes with 22.7% carriage rate, which was lower than at least four novel, uncultured gut phages found in the GVD (Figure 4.13b). Importantly, the host carriage rates of crAssphage were very low in neonatal (0.2%) and infancy (5.6%) samples, which supported previous claims that crAssphage was rarely acquired in early life (Lim *et al.*, 2015; Liang *et al.*, 2016). Although, the crAssphage acquisition pattern seemed to vary by cohorts as recent MAG studies had reported contradictory findings (McCann *et al.*, 2018; Edwards *et al.*, 2019).

Whilst the uncultured, novel phages were widespread in the adult gut virome, the infancy and neonatal gut viromes were dominated by well-characterised cultured phages (Figure 4.13b). Based on publicly available bacterial host information, the most dominant bacterial hosts belonged to the phylum *Firmicutes* (52.5%), which was more than 2-fold the next most abundant identified host phyla *Proteobacteria* and *Bacteroidota* (Figure 4.14a). The prevalence of *Firmicutes* phages was consistent with its predominance among bacterial MAGs (57.4%) and the public gut virome database (Gregory *et al.*, 2019). For 7,162 RefSeq cultured phages with predicted host genera and/or species information, the genus *Escherichia* was the prime host for the adult gut phages (Figure 4.14b). In contrast, the neonatal gut phages exhibited more diverse host ranges with higher frequency in the environmentally-associated *Firmicutes* taxa, including *Staphylococcus*, *Streptococcus*, *E. faecalis* and *C. perfringens*, which were coincidently among the most common MAG species recovered from the neonatal samples (Figure 4.6). Taken together, these results suggested that the neonatal gut viromes were likely shaped by the neonatal gut microbiota (Lim *et al.*, 2015; Shkoporov *et al.*, 2019b), in which the common bacterial colonisers were frequently infected by well-characterised, cultured phages.

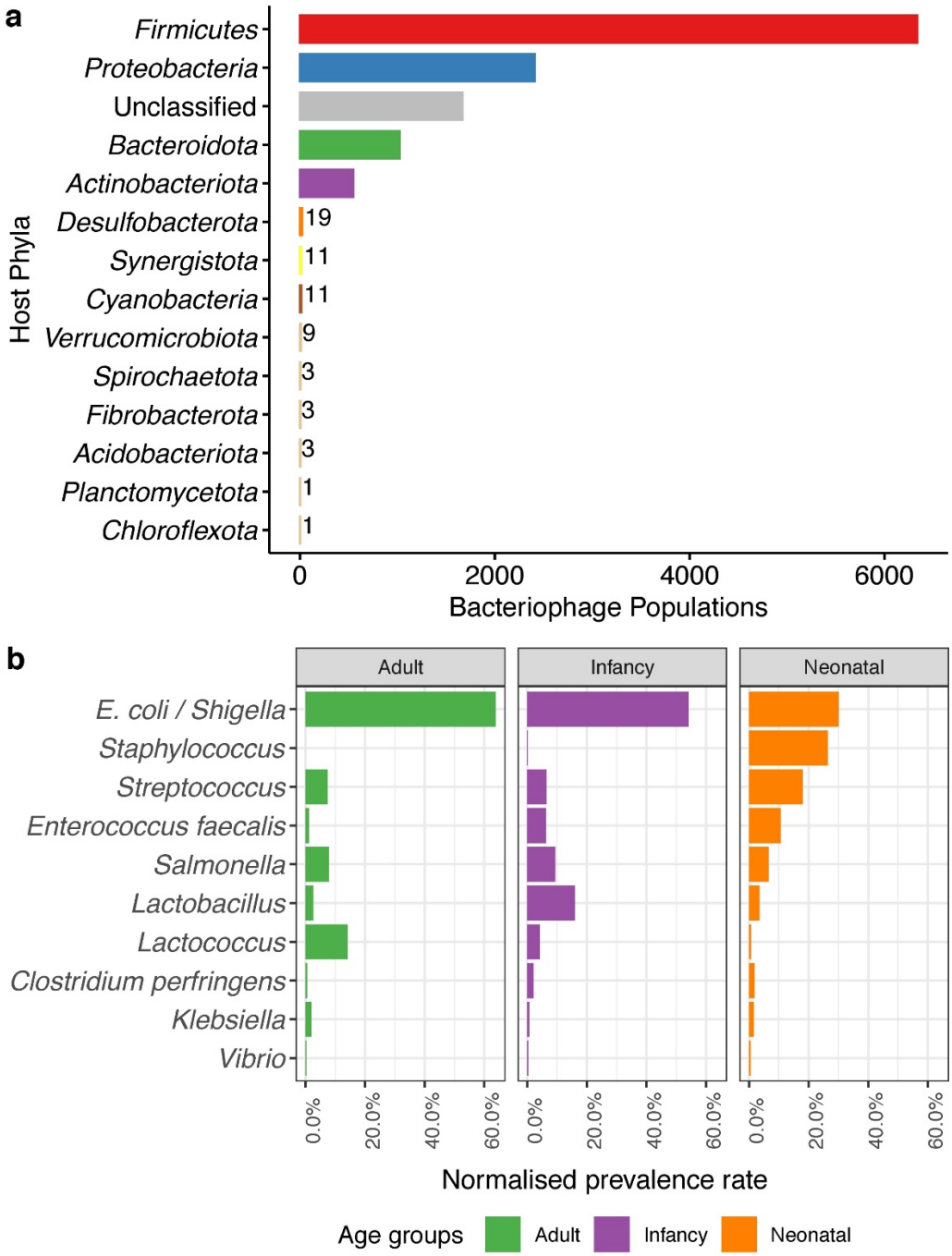

Figure 4.14 Predicted bacterial hosts of the gut phages.

a, Bar plot showing the number of predicted bacterial host phyla of the classified bacteriophage populations with host information (n = 12,067). *Firmicutes*, n = 6,333; *Preoteobacteria*, n = 2,413; Unclassified, n = 1,690; *Bacteroidota*, n = 1,022; *Actinobacteriota*, n = 509. **b,** Bar chart showing the prevalence of the ten most common host for the classified bacteriophages across age groups. Only 7,162 bacteriophages with available predicted host genera (total predicted genera: 52) information were shown. The prevalence rate was normalised by the sum of bacteriophages per age group. The species name was shown if it was the only matching species under the corresponding genus.

4.3.5 Cohort-specific genome catalogue enabled classification of the entire microbiota.

Having so far assembled a catalogue of bacterial, archaeal and eukaryotic genomes from the BBS gut metagenomes, I then sought to determine to which degree these new reference genomes could resolve the unclassified metagenomes. A customised Kraken database consisted of 13,009 high-quality prokaryotic MAGs (pMAGs) enabled classification of 98.3% (IQR = 98.8-99.8%) of the metagenomic sequences across all samples, in which almost the entire (mean 99.3%, IQR 99.5-99.9%) neonatal gut metagenomes could be classified (Figure 4.15). These results represented an overall improvement of 12.9% in the classified metagenome proportion over using the HGG as a reference database, with the most noticeable 27% improvement made in adult samples, followed by 11.5% and 11.6% in the infancy and neonatal samples, respectively.

Critically, using pMAGs exclusive to the BBS dataset as reference genomes outperformed a state-of-the-art reference database consisted of the most comprehensive collection of human gut microbiota-derived cultured isolate and uncultured genomes (HGG+CGR+UMGS) by an average margin of 6.7% across all samples, and up to 7.7% in the neonatal samples (Figure 4.15). This result highlights the important value of cohort-specific metagenome assemblies in unveiling otherwise unexplored, novel microbiota taxa exclusive to the study population.

Inclusion of the HGG genomes and eukaryotic MAGs (eMAGs) could further improve taxonomic classification, although their benefit seemed to be marginal and likely depended on the nature of the microbiota. For example, several neonatal samples were dominated by high abundance eukaryotes, which is extremely rare among healthy adult gut metagenomes. Therefore, eMAGs could be more valuable for taxonomic classification of the neonatal metagenomes. Indeed, the best classification result was achieved when using a combined set of the prokaryotic, eukaryotic MAGs and isolate genomes (HGG), enabling a maximum classification rate of 99.6% (IQR = 99.6-99.9%).

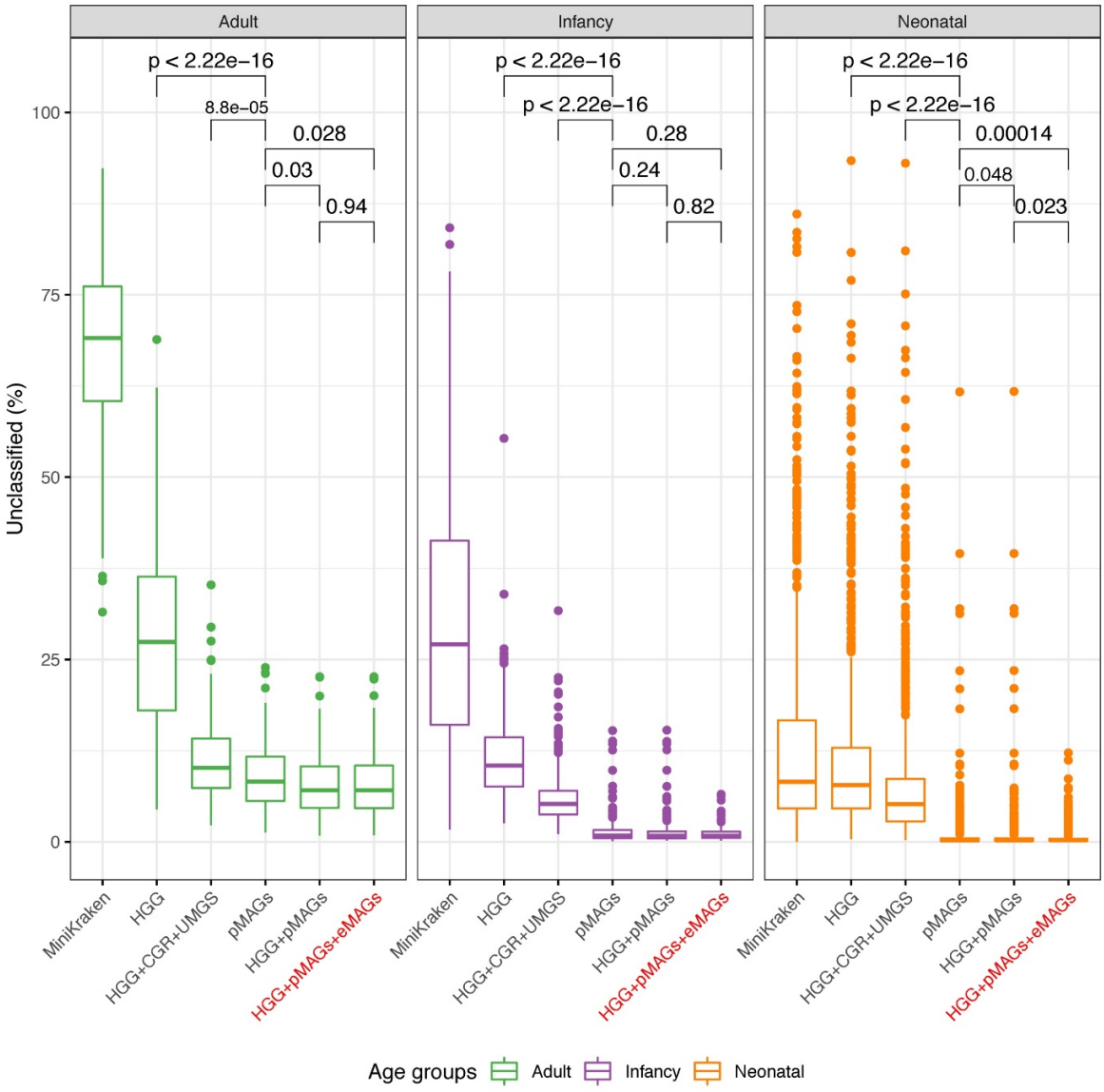

Figure 4.15 Classification of the entire gut metagenomes with cohort-specific MAGs.

Substantial improvement in Kraken classification performance of the BBS MAGs reference databases, in comparison to the study reference database (HGG) and a comprehensive, high-quality gut microbiota reference genome database (HGG+CGR+UMGS, *n* = 4,826) consisted of culture isolate genomes (HGG, *n* = 1,354 and CGR, *n* = 1,520) and novel MAGs recovered from in public datasets (UMGS, *n* = 1,952). Significant reduction in the proportion of unclassified reads was observed in samples across age groups when using only the BBS prokaryotic MAGs (pMAGs, *n* = 13,009). Further improvement in Kraken classification could be achieved by complementing pMAGs with HGG isolate genomes (HGG+pMAGs, *n* = 14,363) in adult and neonatal samples, and additionally with eukaryotic MAGs (HGG+pMAGs+eMAGs, *n* = 14,409, red) in neonatal samples. MiniKraken classification results were shown as background reference. Number of samples in the three age groups: adult (*n* = 175, green), infancy (*n* = 302, purple), neonatal (*n* = 1,202, orange). Statistical comparisons between group means were performed by two-sided Wilcoxon rank-sum tests.

4.4 Conclusions

Undertaking single-sample assembly of 1,679 BBS gut metagenomes, I have successfully reconstructed a comprehensive catalogue comprising 13,009 near-complete microbial genomes corresponding to 654 known species and 138 novel taxa (Figure 4.16). To uncover the most neglected members of the gut microbial communities, I also recovered 21,639 unique viral populations, of which 83.6% were novel, uncultivated phages; as well as the gut 'eukaryome' represented by 18 fungal species and intestinal eukaryotic parasites *Cyclospora cayetanensis* and *Blastocystis*. The genomes matched to known, prevalent bacterial species distributed in accordance to age groups and delivery modes, which confirmed previous observations in assembly-independent metagenomic analyses.

To my knowledge, this work represents the largest ever metagenomic assembly effort based on a single human gut microbiota cohort. The improved genome resource represents a 63.8% expansion of previously unexplored microbial diversity, and an improvement of 12.9% in taxonomic classification rates over the use of isolate genomes. Notably, most of this expanded microbial diversity resided in rare, non-core taxa usually only found in adult gut microbiotas. Having recapitulated the specific and novel taxa in the study population, the newly recovered genomes captured the 6.7% hidden diversity otherwise inaccessible with public gut microbiota genomes. Finally, an integrated catalogue of high-quality reference genomes, from pure cultures and metagenomic assemblies enabled an unprecedented 99.6% classification of the neonatal gut microbiota, in comparison to the current best record of 87.51% using 235,713 reference genomes (Pasolli *et al.*, 2019). These results highlighted the importance of cohort-specific genome catalogues to enable precision metagenomics and future cultivation-free, comparative genomics of taxa associated with important species and strain-specific functions in the early-life gut microbiota (e.g. *Bifidobacterium* sp.) in population-based studies, which would be of crucial value in non-Western cohorts with much more unknown microbial diversity.

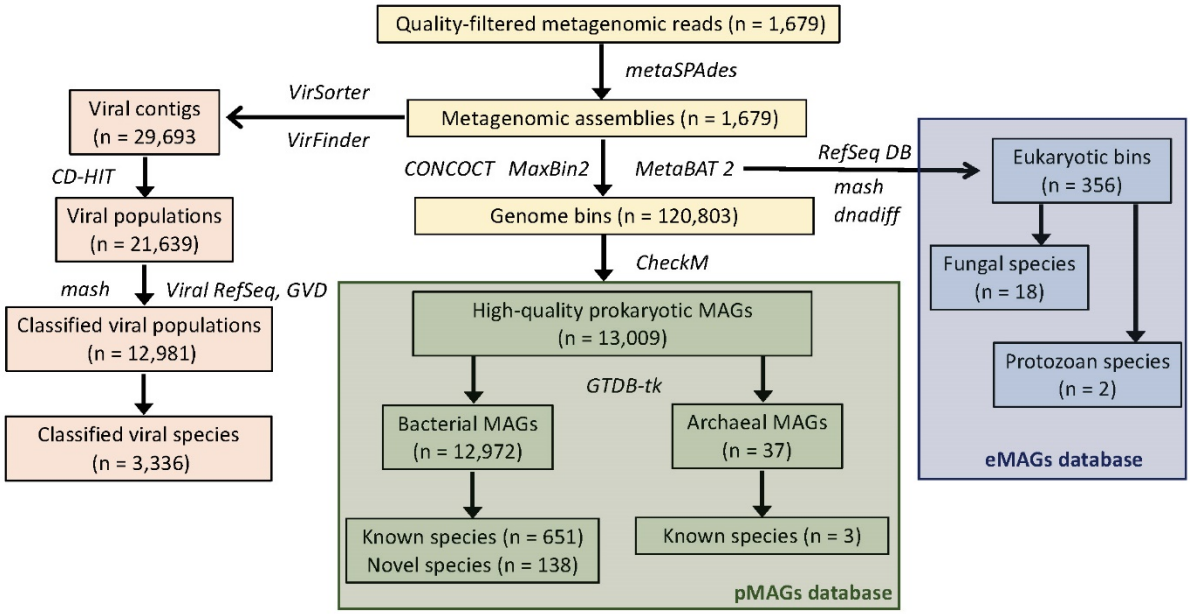

Figure 4.16 Schematic overview of genome recovery and taxonomic identification. Software and database names appeared italicised in the relevant steps.

Chapter 5: Summary and future work

In this Thesis, I generated and analysed the largest datasets of shotgun metagenomes, isolate genomes and metagenome-assembled genomes of the neonatal gut microbiota to date.

In Chapter 2, I performed species and strain-level metagenomic characterisation of longitudinal samples to uncover the temporal dynamics in the gut microbiota during very early life. Cross-sectional analyses of the microbiota composition, and the pattern of maternal microbiota transmission of hundreds of individuals enabled me to establish the dominant effect of delivery mode. Primary colonisers associated with delivery modes shaped the gut microbial communities in the earliest first phase of microbiota development, with a diminished effect that persists into infancy. This observation resonated with the recent findings regarding the significant and persisting effect of delivery mode in the first three years of life (Wampach *et al.*, 2018; Stewart *et al.*, 2018; Vatanen et al., 2018). My work also emphasises the role of the mother's gut bacteria, rather than vaginal bacteria in priming the neonatal gut microbiota, which calls into question the controversial "vaginal seeding" practice.

The other major novel discovery in Chapter 2 was the finding of a stunted neonatal gut microbiota profile as characterised by the delayed colonisation of commensal, maternally-transmitted bacteria and the high-level colonisation of non-enteric bacteria including opportunistic pathogens in the hospital environment. The striking observation that nearly half of the vaginally delivered babies shared the similar, albeit weaker microbiota perturbation pattern (low-*Bacteroides* and enriched pathogen carriage) with those delivered by caesarean section indicate that the mode of delivery was not, *per se*, the only determining factor of the gut microbiota assembly process. In comparison to other perinatal factors in hospital births (i.e. maternal intrapartum antibiotic prophylaxis, postnatal antibiotics and duration of hospital stay) that exhibited smaller effect on the gut microbiota, the mode of delivery is the one most likely to pre-determine the composition of the local bacterial species pool when a newborn baby

makes the first and largest exposure to the immediate, surrounding environment. Given the striking pattern of maternal strain transmission by modes of delivery, I hypothesise that vaginal delivery strongly promotes the inclusion of maternal gut bacteria in the local species pool by facilitating the neonatal exposure of faecal-oral microbiota contact through the birth canal, whereas multitude of perinatal factors in hospital births alters the local species pool by completely depriving (e.g. caesarean section) or reducing the exposure of maternal microbiota (e.g. antibiotics) (Figure 5.1). This highlights the need for future birth cohort studies that also sample home births (Combellick *et al.*, 2018) to better understand the consequence of the perinatal factors in hospital births.

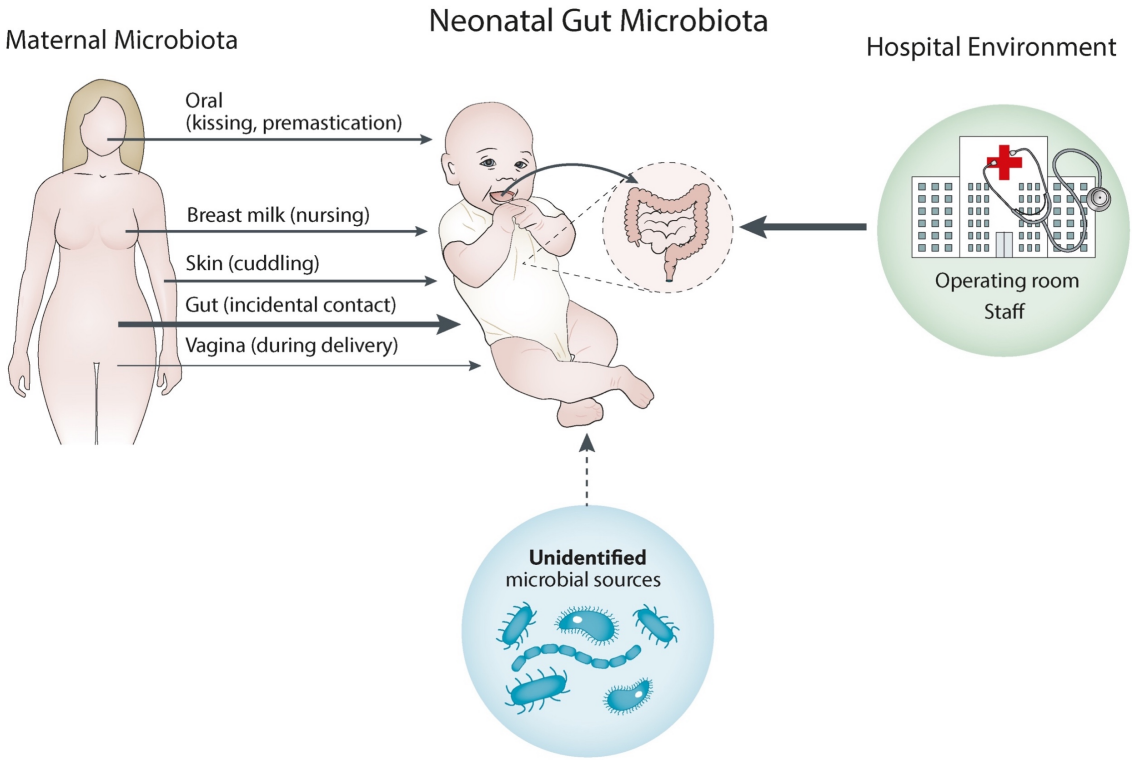

Figure 5.1 Local species pools available for colonisation of the gut microbiota in hospital births.

At birth, babies were immediately exposed to pools of microorganisms from the surrounding environment, which could potentially colonise and establish in the neonatal gut microbiota. These included the maternal microbiota, in which the gut bacteria are exposed to the newborn baby through the incidental faecal-oral contact during vaginal delivery; and the hospital environmental microbiota in the operating room and from medical personnel and birth attendant; and yet unknown sources. The thickness of the arrows denotes the hypothesised relative contributions of microorganisms from different sources that could colonise and establish in the neonatal gut microbiota. Adapted from Sprockett *et al.*, 2018.

The surprising and alarming observation of high-level opportunistic pathogen carriage was further investigated in Chapter 3, in which I performed additional metagenomic analysis and experimental validation through large-scale targeted culturing. This work showed that the disrupted transmission of the maternal gastrointestinal bacteria (particularly pioneering *Bacteroides* species) through delivery by caesarean section and maternal intrapartum antibiotic prophylaxis predisposed newborn babies to extensive and frequency colonisation by clinically important opportunistic pathogens. This perturbation pattern was previously frequently reported among preterm hospitalised babies, but overlooked in previous full-term, healthy cohorts due to insufficient statistical power (Section 3.3.5). Subsequent whole-genome sequence analysis of hundreds of the cultured opportunistic pathogen strains provided critical insights into their population structure and pathogenicity potential with higher resolution than can be achieved by using shotgun metagenomics. This analysis confirmed that the opportunistic pathogen colonisers in the neonatal gut were neither acquired from their mothers nor high-risk lineages, but mostly representative of the highly diverse opportunistic pathogen populations currently circulating in hospitals and among asymptomatic carriers in the UK. Although the prevalent colonisation of opportunistic pathogens in the BBS babies was asymptomatic, the defining feature of these AMR-containing bacteria is their capacity to cause infections in immunologically compromised hosts (Price *et al.*, 2017), which in this context represents a risk factor to neonates and infants in a critical window of immune development. Given the expected differential immunogenic properties of the commensal and opportunistic pathogen colonisers (Vatanen *et al.*, 2016), the consequences of the lack of commensal colonisation and/or opportunistic pathogen carriage in very early life should be further monitored through long-term samplings of both the microbiota and immune system development (Olin *et al.*, 2018).

The frequent asymptomatic gastrointestinal carriage of opportunistic pathogens highlighted herein also has significant implications for their surveillance and control of the underlying infection reservoir. Future birth cohort studies should consider sampling the microbiotas within

the hospital environment (e.g. operating room, neonatal unit, staff) to elucidate the exact sources and hotspots of opportunistic pathogens (Lax *et al.*, 2017). Although long been viewed to act as both commensals and pathogens, our current knowledge of genetics and epidemiology driving the pathogen-commensal continuum in *Enterococcus*, *Klebsiella* and *Enterobacter* species predominantly came from studying infection isolates, with hugely disproportional sampling bias towards hypervirulent and multi-drug resistant (MDR) strains. This issue was highlighted in the whole-genome sequence analysis presented in Chapter 3 that was evident by the paucity of publicly available commensal gastrointestinal-derived genomes (*E. faecalis*, n = 28; *Enterobacter* spp. and *Klebsiella* spp.; n = 37). We are witnessing a paradigm shift in our understanding of pathogens in the context of the host microbiota (Vayssier-Taussat *et al.*, 2014). The gastrointestinal carriage of opportunistic pathogens is increasingly recognised as a risk factor and a major reservoir for hospital-associated infections (Tamburini *et al.*, 2018), whereas the within-hospital transmission of MDR strains overpopulating the current public genome database only represent a small burden of opportunistic infections (Gorrie *et al.*, 2017). In this regard, the number of commensal genomes generated in this study (*E. faecalis*, n = 356; *Enterobacter* spp. and *Klebsiella* spp.; n = 280) expands the commensal populations of these species by several orders of magnitudes, which should become a valuable resource for future population genomics studies that aim to investigate the genetic basis underlying the success of asymptomatic colonisation and transition from asymptomatic colonisation to infection.

In summary, the findings presented in the first two chapters contribute to our understanding that colonisation of the human gut microbiota is initiated at the time of birth and shaped by the exposure to the surrounding environment (i.e. mother and hospital). Together with the recent studies debunking microbiota colonisation *in utero* in healthy pregnancy (de Goffau *et al.*, 2019; Theis *et al.*, 2019), the field is now presented with conclusive evidence to settle controversies regarding when the human gut microbiota is established (Aagaard *et al.*, 2014), and the roles of

delivery mode (Chu *et al.*, 2017) and maternal microbiota (Dominguez-Bello *et al.*, 2010; 2016) during this process.

There are, inevitably, technical limitations to this study that could have been addressed in future studies. Although the sample storage protocol (no preservation buffer for room temperature and 4-°C storage) was shown to be robust to technical variation in microbiome measurements at the time of study design (discussed in 2.3.8), it was not ideal for large multi-centre microbiome cohort. State-of-the-art preservation methods should be used to minimize the potential effect of sample storage on the microbiota composition (Vandeputte *et al.,* 2017). Furthermore, the DNA extraction protocol (i.e. choice of bead-beating and lysis buffer) was designed for targeting bacterial DNA, which could explain the depletion of archaeal, fungal and eukaryotic DNA as observed in the MAGs. Future studies interested in the understudied, non-bacterial communities should perform pilot experiments testing the efficacy and yield of different DNA storage and extraction protocols in the study design phase. In addition, studies that primarily focus on the abundances of microbial markers (e.g. pathogens in disease and cancer patients) should strongly consider incorporating quantitative methods into their sample processing and analysis workflows. Finally, the sampling window of this study missed out on revealing the microbiota developmental dynamics between birth and day 4 of life, which remains understudied in literature and should be addressed in future cohorts by sampling all babies at birth (meconium).

Whilst this work has elucidated the significant impact of perinatal factors on the neonatal gut microbiota, it remains to be determined if the perturbed composition, and/or the lack of maternal gut bacteria in the neonatal gut microbiota negatively affect health outcomes in childhood and later life. This warrants further investigations in long-term population-based birth cohorts such as the BBS, which aims at recruiting tens of thousands of children at birth with long-term health outcome followed-up. Given the sparse and over-dispersed nature of the neonatal gut metagenome observed in this study, I estimated that a recruitment sample size of 40,000 is

required to provide adequate statistical power to detect small changes (~10%) in the most abundant gut microbiota species using a nested case-control design for key clinical outcomes with expected prevalence of around 10% at age 5 (e.g. asthma). However, other than the prevailing lack of statistical power applicable to all microbiome studies, the fact that no birth cohort to date has been able to establish a causal link between any microbiota marker with later onset of disease in human is likely a manifestation of the general lack of mechanistic understanding between any microbiome markers (e.g. diversity, taxa, genes) and host health (function, phenotype) (Fischbach, 2018).

One approach that is particularly applicable to dissecting the host-microbiota interactions in the context of neonatal gut microbiota is by using germ-free mice to recapitulate the initial colonisation by the gut microbiota. They represent a powerful *in vivo* model system with controlled host genetic background, and have been successfully utilised in previous infant gut microbiota studies in validating potential microbiome markers of host phenotypes (Smith *et al.*, 2013; Arrieta *et al.*, 2015; Noval Rivas *et al.*, 2013), screening colonisation resistance in commensal bacteria (Kim *et al.*, 2017; Feehley *et al.*, 2019; Mullineaux-Sanders *et al.*, 2018), and elucidating priority effects of colonisation order (Martínez *et al.*, 2018). Importantly, it is worth noting that nonhuman primate models had also been established to study host diet-microbiota interactions, which could provide a better experimental system for future human microbiome studies (Ma *et al.*, 2014; Amato *et al.*, 2015).

Looking ahead, the next step of the BBS will involve utilising the BBS culture collection and germ-free mice to perform *in vivo* characterisation of the immunogenic and colonisation resistance properties of the primary colonising commensal strains identified in the BBS, including the priority effects of the commensal *Bacteroides* strains which appeared to exhibit time and order-dependent colonisation patterns. The aim of these experiments is to characterise the functional impact of microbiota perturbation to the immune systems in mouse models, which should provide mechanistic insights on how the early colonising bacteria mediate

immune regulation. Ultimately, these experiments could facilitate efforts to identify a defined mixture of strains that restore the perturbed neonatal microbiota in early life.

State-of-the-art, reference-based taxonomic profiling of the gut metagenomes is inherently limited by the availability of reference genomes representing catalogued microbial diversity, leaving a considerable fraction of the microbiome taxa that usually could not be classified and thus remained left unexplored (which was shown to be more of an issue for the adult than neonatal gut metagenomes). In Chapter 4, I performed a comprehensive genomic survey of the hidden microbial diversity in the BBS gut microbiotas through the large-scale metagenomic assembly. This work substantially improves our knowledge of the entire prokaryotic, eukaryotic and viral diversity in the neonatal gut microbiome, and more importantly, the resulting BBS MAGs collection enables an unprecedented classification of almost the entirety of the BBS neonatal gut metagenome. Based on this result, I reason that the generation of a cohort-specific MAGs collection cataloguing the hidden taxa and strain-level diversity unique to the study population should greatly reduce the faction of inaccessible taxa, and should therefore be preferentially utilised, in combination with public genomes in future population-based metagenomics studies.

In this Thesis, I have primarily focused on characterising the gut microbial communities taxonomically; one notable omission was the characterisation of the functional potential encoded in gut metagenomes. This was due to technical reasons considering the limited utilities of the current functional prediction approach (to permit meaningful comparative analyses), which is one of the main technical limitation in the field of metagenomics today (Thomas, Segata, 2019). The lack of classification and annotation for most accessory genes means that popular computational tools such as HUMAnN (Abubucker *et al.*, 2012) will be inevitably biased towards the highly conserved core pathways and functions (Quince *et al.*, 2017).

Nevertheless, the BBS MAGs collection generated in Chapter 4 will serve as a valuable resource in future population and comparative genomics analyses, which will aim to elucidate

the otherwise inaccessible phylogenetic and functional diversity in prevalent taxa and dominant colonisers in the neonatal gut. The obvious candidates to start with are members of the *Bifidobacterium* (1,467 MAGs represented by 15 species, including one novel species) and *Bacteroides* genera (1,037 MAGs represented by 37 species and seven novel species), both of which are known dominant members of the early-life microbiota with important functional roles. Analysis of these diverse collections of MAGs should provide new insights into the genetic factors driving the species and strain-specific functions of human milk oligosaccharides (HMOs) metabolism (Matsuki *et al.*, 2016; Vatanen et al., 2019) and immune modulation (O'Neill *et al.*, 2017; Vatanen *et al.*, 2018).

Future detailed characterization is needed to improve our understanding of the early-life gut virome, which remains underexplored in spite of the recent advances in the adult gut virome (Garmaeva *et al.*, 2019). The identification, classification and phylogenetic analyses of the novel and unknown bacteriophages, in particular the crAssphage, could be improved by using other major databases of the gut viromes including IMG/VR (Paez-Espino *et al.,* 2017; Shkoporov *et al.*, 2019a; Guerrero *et al.*, unpublished) and crAss-like phages (Guerin *et al.,* 2018; Edwards *et al.,* 2019); as well as more advanced computational tools, including machine learning-based viral sequence prediction (Ren *et al*., 2018; Tampuu *et al*., 2019), network-based classification of prokaryotic viruses (Jang *et al*., 2019) and CRISPR spacer-based bacterial host prediction (Edgar *et al*., 2007). Finally, the longitudinal collection of both isolate genomes and MAGs of the opportunistic pathogen species would permit better quality assessment of MAGs, and also present exciting opportunities to further interrogate the dynamics of intra-host multiple-strain colonisation, dominant-strain replacement and inter-host strain transmission.

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Appendices

Appendix 1 StrainPhlAn species and genomes

The table include a list of species and genomes used to generate mash distance-based phylogenetic trees in Figure 2.12. Reference genomes were extracted from the StrainPhlAn database (metaphlan2/utils/species2genomes.txt)

Species names	Genome accessions
Streptococcus vestibularis	GCF_000180075
Streptococcus thermophilus	GCF_000011825
Streptococcus salivarius	GCF_000225385
Streptococcus parasanguinis	GCF_000260695
Parabacteroides merdae	GCF_000154105
Parabacteroides distasonis	GCF_000012845
Escherichia coli	GCF_000457635
Collinsella aerofaciens	GCF_000169035
Bifidobacterium pseudocatenulatum	GCF_000173435
Bifidobacterium longum	GCF_000261265
Bifidobacterium bifidum	GCF_000155395
Bifidobacterium adolescentis	GCF_000154085
Bacteroides xylanisolvens	GCF_000273315
Bacteroides vulgatus	GCF_000273295
Bacteroides uniformis	GCF_000403175
Bacteroides thetaiotaomicron	GCF_000403155
Bacteroides ovatus	GCF_000273195
Bacteroides fragilis	GCF_000009925
Bacteroides dorei	GCF_000273035
Ruminococcus_torques	GCF_000153925
Blautia wexlerae	GCF_000159975
Faecalibacterium_prausnitzii	GCF_000166035

Appendix 2 Clinical metadata of the BBS participants

The table contains the complete clinical metadata of the 1,679 gut metagenomes in this study.

Accession	Individual	Time_point	Delivery_mode	C_Section_type	Late_infancy_sampling_age_months	Days_in_hospital	Hospital	Hospital_destination_after_birth	Gender	Mother_age	Birth weight in 100 grams	Feeding_method	Breastfeeding status	Feeding_breastfed_1hr_birth	Abx_CS_prophylactic	Abx_mother_prior_birth	Abx_mother_labour_IAP	Abx_mother_after_hospital	Abx_Baby_in_hospital	Abx_Baby_after_discharge	Bacteroides_cat	WGS_reads_raw	WGS_reads_trimmed
ERS3420736	512120	4	Caesarean	Elective_CS	Neonatal	1	A	NA	Male	NA	3400	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	3E+07	2.9E+07
ERS3420737	512120	7	Caesarean	Elective_CS	Neonatal	1	A	NA	Male	NA	3400	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	2.6E+07	2.5E+07
ERS3420738	512120	9	Caesarean	Elective_CS	Neonatal	1	A	NA	Male	NA	3400	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	3E+07	2.9E+07
ERS3420739	512120	12	Caesarean	Elective_CS	Neonatal	1	A	NA	Male	NA	3400	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	1.7E+07	1.6E+07
ERS3420740	512120	21	Caesarean	Elective_CS	Neonatal	1	A	NA	Male	NA	3400	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	2E+07	1.9E+07
ERS3420741	513122	4	Vaginal	Vaginal	Neonatal	2	A	NA	Female	NA	3900	NA	NA	NA	NA	no	no	no	no	NA	normal_Bacteroides	3E+07	2.8E+07
ERS3420742	513122	6	Vaginal	Vaginal	Neonatal	2	A	NA	Female	NA	3900	NA	NA	NA	NA	no	no	no	no	NA	normal_Bacteroides	2.5E+07	2.4E+07
ERS3420743	513122	10	Vaginal	Vaginal	Neonatal	2	A	NA	Female	NA	3900	NA	NA	NA	NA	no	no	no	no	NA	normal_Bacteroides	2.6E+07	2.5E+07
ERS3420744	513122	12	Vaginal	Vaginal	Neonatal	2	A	NA	Female	NA	3900	NA	NA	NA	NA	no	no	no	no	NA	normal_Bacteroides	2E+07	1.9E+07
ERS3420745	513122	21	Vaginal	Vaginal	Neonatal	2	A	NA	Female	NA	3900	NA	NA	NA	NA	no	no	no	no	NA	normal_Bacteroides	1.9E+07	1.8E+07
ERS3420746	513122	Mother	Vaginal	Vaginal	Mother	2	A	NA	Female	NA	3900	NA	NA	NA	NA	no	no	no	no	NA	NA	5.5E+07	5.2E+07
ERS3420747	514123	4	Vaginal	Vaginal	Neonatal	4	A	NA	Male	NA	3400	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	3.2E+07	3E+07
ERS3420748	514123	7	Vaginal	Vaginal	Neonatal	4	A	NA	Male	NA	3400	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	3.5E+07	3.3E+07
ERS3420749	514123	12	Vaginal	Vaginal	Neonatal	4	A	NA	Male	NA	3400	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	3.1E+07	2.9E+07
ERS3420750	514123	14	Vaginal	Vaginal	Neonatal	4	A	NA	Male	NA	3400	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	4E+07	3.8E+07
ERS3420751	514124	4	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	1.4E+07	1.4E+07
ERS3420752	514124	6	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	2.4E+07	2.3E+07
ERS3420753	514124	7	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	3E+07	2.8E+07
ERS3420754	514124	8	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	3.1E+07	3E+07
ERS3420755	514124	Mother	Vaginal	Vaginal	Mother	0	A	NA	Female	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	NA	6.6E+07	6.3E+07
ERS3420756	515126	Mother	Vaginal	Vaginal	Mother	1	A	NA	Female	NA	3300	NA	NA	NA	NA	no	NA	no	no	NA	NA	5.8E+07	5.5E+07
ERS3420757	515126	4	Vaginal	Vaginal	Neonatal	1	A	NA	Female	NA	3300	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	3.3E+07	3E+07
ERS3420758	515126	7	Vaginal	Vaginal	Neonatal	1	A	NA	Female	NA	3300	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3420759	515126	10	Vaginal	Vaginal	Neonatal	1	A	NA	Female	NA	3300	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	3.1E+07	2.9E+07
ERS3420760	515126	11	Vaginal	Vaginal	Neonatal	1	A	NA	Female	NA	3300	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	2.9E+07	2.7E+07
ERS3420761	515126	21	Vaginal	Vaginal	Neonatal	1	A	NA	Female	NA	3300	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	2.3E+07	2.1E+07
ERS3420762	515127	Mother	Vaginal	Vaginal	Mother	2	A	NA	Male	NA	3600	NA	NA	NA	NA	no	NA	no	no	NA	NA	5.5E+07	5.2E+07
ERS3420763	515127	7	Vaginal	Vaginal	Neonatal	2	A	NA	Male	NA	3600	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	2.8E+07	2.6E+07
ERS3420764	519128	Mother	Caesarean	Elective_CS	Mother	2	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	NA	5.9E+07	5.6E+07
ERS3420765	519128	4	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	3.5E+07	3.2E+07
ERS3420766	519128	7	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	2.7E+07	2.5E+07
ERS3420767	519128	12	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	3.1E+07	2.8E+07
ERS3420768	519128	14	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	3E+07	2.8E+07
ERS3420769	519128	18	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	2.7E+07	2.5E+07
ERS3420770	519128	21	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	3.2E+07	3E+07
ERS3420771	519129	4	Caesarean	Elective_CS	Neonatal	1	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	2.8E+07	2.7E+07
ERS3420772	519129	7	Caesarean	Elective_CS	Neonatal	1	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	3.1E+07	3E+07
ERS3420773	519129	12	Caesarean	Elective_CS	Neonatal	1	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	2.8E+07	2.6E+07
ERS3420774	519129	14	Caesarean	Elective_CS	Neonatal	1	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	3.4E+07	3.2E+07
ERS3420775	519129	21	Caesarean	Elective_CS	Neonatal	1	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	1.9E+07	1.8E+07
ERS3420776	519129	Mother	Caesarean	Elective_CS	Mother	1	A	NA	Female	NA	3500	NA	NA	NA	Yes	no	NA	no	no	NA	NA	5.8E+07	5.5E+07
ERS3420777	521130	4	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	2900	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	2.8E+07	2.6E+07
ERS3420778	521130	10	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	2900	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	3.2E+07	3E+07
ERS3420779	521130	12	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	2900	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	3.3E+07	3.1E+07
ERS3420780	521130	21	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	2900	NA	NA	NA	NA	no	NA	no	no	NA	normal_Bacteroides	3.3E+07	3.1E+07
ERS3420781	521130	Mother	Vaginal	Vaginal	Mother	0	A	NA	Female	NA	2900	NA	NA	NA	NA	no	NA	no	no	NA	NA	5.8E+07	5.5E+07
ERS3420782	523133	7	Vaginal	Vaginal	Neonatal	0	A	NA	Male	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	3.1E+07	2.9E+07
ERS3420783	523133	9	Vaginal	Vaginal	Neonatal	0	A	NA	Male	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	3.4E+07	3.3E+07
ERS3420784	523133	11	Vaginal	Vaginal	Neonatal	0	A	NA	Male	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	2.8E+07	2.6E+07
ERS3420785	523133	13	Vaginal	Vaginal	Neonatal	0	A	NA	Male	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	3.5E+07	3.3E+07
ERS3420786	523133	4	Vaginal	Vaginal	Neonatal	0	A	NA	Male	NA	3200	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	3.3E+07	3.1E+07
ERS3420796	604136	Mother	Vaginal	Vaginal	Mother	0	A	NA	Female	NA	3900	NA	NA	NA	NA	no	NA	no	no	NA	NA	5.3E+07	5E+07
ERS3420797	604136	7	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	3900	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3420798	604136	10	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	3900	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	3.2E+07	2.9E+07
ERS3420799	604136	11	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	3900	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	2.5E+07	2.3E+07
ERS3420800	604136	14	Vaginal	Vaginal	Neonatal	0	A	NA	Female	NA	3900	NA	NA	NA	NA	no	NA	no	no	NA	low_Bacteroides	2E+07	1.9E+07
ERS3420801	606141	4	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3800	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	2.9E+07	2.9E+07
ERS3420802	606141	7	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3800	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	1.8E+07	1.7E+07
ERS3420803	606141	8	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3800	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	3E+07	2.9E+07
ERS3420787	606141	10	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3800	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	1.7E+07	1.6E+07
ERS3420788	606141	12	Caesarean	Elective_CS	Neonatal	2	A	NA	Female	NA	3800	NA	NA	NA	Yes	no	NA	no	no	NA	low_Bacteroides	5469398	5206596
ERS3420789	606141	Mother	Caesarean	Elective_CS	Mother	2	A	NA	Female	NA	3800	NA	NA	NA	Yes	no	NA	no	no	NA	NA	6.2E+07	5.9E+07
ERS3420790	BBS0001	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	1.8E+07	1.7E+07
ERS3420791	BBS0003	17	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	1.5E+07	1.4E+07
ERS3420792	BBS0006	12	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.8E+07	2.5E+07
ERS3420793	BBS0006	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3420794	BBS0007	10	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	3.8E+07	3.6E+07
ERS3420795	BBS0008	10	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3420804	BBS0011	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3420805	BBS0014	11	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.4E+07	2E+07
ERS3420806	BBS0014	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3420807	BBS0024	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3420808	BBS0024	Mother	Caesarean	Elective_CS	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.3E+07	1.9E+07
ERS3420809	BBS0035	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3420810	BBS0038	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.4E+07	2.1E+07
ERS3420811	BBS0038	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3420812	BBS0045	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2E+07	1.8E+07
ERS3420813	BBS0045	21	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3420814	BBS0048	4	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3420815	BBS0048	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3420816	BBS0048	21	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3420817	BBS0051	4	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3420818	BBS0051	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3420819	BBS0051	21	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3420820	BBS0055	13	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3420821	BBS0055	21	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3420822	BBS0057	4	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.2E+07	2E+07
ERS3420823	BBS0057	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3420824	BBS0057	21	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3420825	BBS0059	4	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3420826	BBS0059	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3420827	BBS0061	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	1.7E+07	1.5E+07
ERS3420828	BBS0062	4	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3420829	BBS0062	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2E+07	1.8E+07
ERS3420830	BBS0067	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3420831	BBS0067	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3420832	BBS0070	4	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	normal_Bacteroides	2E+07	1.7E+07

ERS3420833	BBS0070	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	normal_Bacteroides	1.7E+07	1.5E+07
ERS3420834	BBS0070	Mother	Caesarean	Elective_CS	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.1E+07	1.8E+07
ERS3420835	BBS0072	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.3E+07	2E+07
ERS3420836	BBS0073	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3420837	BBS0074	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.3E+07	2E+07
ERS3420838	BBS0075	4	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	No	no	Yes	no	NA	NA	low_Bacteroides	2.5E+07	2.3E+07
ERS3420839	BBS0075	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	No	no	Yes	no	NA	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3420840	A00021_T2	4	Caesarean	Elective_CS	Neonatal	5	A	Postnatal	Female	NA	2400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3420841	A00021_T2	7	Caesarean	Elective_CS	Neonatal	5	A	Postnatal	Female	NA	2400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3420842	A00021_T1	21	Caesarean	Elective_CS	Neonatal	5	A	Postnatal	Female	NA	2400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3420843	A00021_T2	21	Caesarean	Elective_CS	Neonatal	5	A	Postnatal	Female	NA	2400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3420844	A00023	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	NA	3000	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3420845	A00031	7	Caesarean	Emergency_	Neonatal	12	A	NICU	Male	NA	3800	NoBF	No	No	Yes	no	No	no	Yes	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3420846	A00031	21	Caesarean	Emergency_	Neonatal	12	A	NICU	Male	NA	3800	NoBF	No	No	Yes	no	No	no	Yes	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3420847	A00043	4	Vaginal	Vaginal	Neonatal	4	A	Postnatal	Male	25-30	3800	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3420848	A00043	7	Vaginal	Vaginal	Neonatal	4	A	Postnatal	Male	25-30	3800	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3420849	A00043	21	Vaginal	Vaginal	Neonatal	4	A	Postnatal	Male	25-30	3800	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3420850	A00044	7	Caesarean	Elective_CS	Neonatal	7	A	NICU	Male	30-35	2900	BF	Yes	No	Yes	no	No	Yes	Yes	Yes	low_Bacteroides	2.3E+07	2.2E+07
ERS3420851	A00044	21	Caesarean	Elective_CS	Neonatal	7	A	NICU	Male	30-35	2900	Mixed	Yes	No	Yes	no	No	no	Yes	No	low_Bacteroides	1.9E+07	1.6E+07
ERS3420852	A00067	7	Vaginal	Vaginal	Neonatal	NA	A	NICU	Female	NA	1300	NA	NA	No	No	no	Yes	no	NA	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3420853	A00067	21	Vaginal	Vaginal	Neonatal	NA	A	NICU	Female	NA	1300	NA	NA	No	No	no	Yes	no	NA	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3420854	A00105	7	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	25-30	3400	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3420855	A00105	21	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	25-30	3400	BF	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.2E+07	1.9E+07
ERS3420856	A00106	Mother	Vaginal	Vaginal	Mother	26	A	NA	Male	30-35	1700	NA	NA	NA	NA	no	NA	no	Yes	NA	NA	2.5E+07	2.2E+07
ERS3420857	A00106_T1	21	Vaginal	Vaginal	Neonatal	26	A	NICU	Male	NA	1700	Mixed	Yes	No	NA	no	NA	no	Yes	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3420858	A00106_T2	21	Vaginal	Vaginal	Neonatal	26	A	NICU	Male	NA	1700	Mixed	Yes	No	NA	no	NA	no	Yes	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3420859	A00134	Mother	Caesarean	Elective_CS	Mother	28	A	NA	Male	45-50	NA	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3420860	A00134	21	Caesarean	Elective_CS	Neonatal	28	A	NICU	Male	45-50	NA	NoBF	No	No	Yes	no	NA	no	NA	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3420861	A00155	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	35-40	2900	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3420862	A00155	Infancy	Caesarean	Elective_CS	12.17	2	A	Postnatal	Male	35-40	2900	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3420863	A00163	Mother	Vaginal	Vaginal	Mother	3	A	NA	Male	35-40	3900	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.7E+07	2.4E+07
ERS3420864	A00163	4	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Male	35-40	3900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.7E+07	2.4E+07
ERS3420865	A00185	Mother	Caesarean	Elective_CS	Mother	1	A	NA	Male	30-35	4800	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.5E+07	2.2E+07
ERS3420866	A00185	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	4800	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3420867	A00185	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	4800	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3420868	A00190	4	Vaginal	Vaginal	Neonatal	1	A	Home	Female	30-35	3400	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3420869	A00190	7	Vaginal	Vaginal	Neonatal	1	A	Home	Female	30-35	3400	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3420870	A00190	21	Vaginal	Vaginal	Neonatal	1	A	Home	Female	30-35	3400	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.5E+07
ERS3420871	A00217	4	Vaginal	Vaginal	Neonatal	0	A	Postnatal	Female	25-30	3100	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	2.1E+07
ERS3420872	A00217	7	Vaginal	Vaginal	Neonatal	0	A	Postnatal	Female	25-30	3100	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.5E+07	2.2E+07
ERS3420873	A00219	4	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	30-35	3500	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3420874	A00219	7	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	30-35	3500	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.5E+07
ERS3420875	A00219	21	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	30-35	3500	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3420876	A00502	21	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Female	35-40	3800	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3420877	A00502	4	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Female	35-40	3800	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.4E+07
ERS3420878	A00502	7	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Female	35-40	3800	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3420879	A00502	Infancy	Vaginal	Vaginal	7.53	3	A	Postnatal	Female	35-40	3800	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3420880	A00539	Mother	Vaginal	Vaginal	Mother	0	A	NA	Female	30-35	3200	NA	NA	NA	No	no	No	no	NA	NA	NA	2.3E+07	1.9E+07
ERS3420881	A00539	7	Vaginal	Vaginal	Neonatal	0	A	Home	Female	30-35	3200	Mixed	Yes	Yes	No	no	No	no	No	NA	low_Bacteroides	2.5E+07	2E+07
ERS3420882	A00541	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3100	BF	Yes	Yes	No	no	No	no	No	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3420883	A00541	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3100	Mixed	Yes	Yes	No	no	No	no	No	NA	low_Bacteroides	1.9E+07	1.3E+07
ERS3420884	A00541	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3100	BF	Yes	Yes	No	no	No	no	No	NA	low_Bacteroides	2E+07	1.4E+07
ERS3420885	A00559	4	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Female	25-30	2500	Mixed	Yes	No	NA	no	Yes	no	No	NA	normal_Bacteroides	3.3E+07	2.8E+07
ERS3420886	A00559	7	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Female	25-30	2500	NA	NA	No	NA	no	Yes	no	No	NA	normal_Bacteroides	2.9E+07	2.4E+07
ERS3420887	A00559	21	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Female	25-30	2500	BF	Yes	No	NA	no	Yes	no	No	NA	normal_Bacteroides	2.5E+07	2.1E+07
ERS3420888	A00570	Mother	Vaginal	Vaginal	Mother	1	A	NA	Male	40-45	3700	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2E+07
ERS3420889	A00570	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	40-45	3700	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.6E+07
ERS3420890	A00570	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	40-45	3700	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3420891	A00574	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3800	BF	Yes	NA	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2E+07
ERS3420892	A00574	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3800	BF	Yes	NA	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3420893	A00574	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3800	BF	Yes	NA	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3420894	A00576	Mother	Vaginal	Vaginal	Mother	1	A	NA	Male	25-30	3600	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.6E+07	2.2E+07
ERS3420895	A00576	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.6E+07
ERS3420896	A00576	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	1.8E+07
ERS3420897	A00576	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3420898	A00908_T1	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	NA	2100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	1.9E+07
ERS3420899	A00908_T1	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	30-35	2100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3420900	A00908	Mother	Caesarean	Elective_CS	Mother	2	A	NA	Female	30-35	2100	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3420901	A00940	Mother	Vaginal	Vaginal	Mother	1	A	NA	Female	40-45	3700	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.7E+07	2.1E+07
ERS3420902	A00940	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Female	40-45	3700	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	2E+07
ERS3420903	A00942	Mother	Vaginal	Vaginal	Mother	1	A	NA	Male	35-40	3400	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	1.9E+07
ERS3420904	A00942	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	35-40	3400	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.1E+07
ERS3420905	A00942	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	35-40	3400	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.1E+07
ERS3420906	A00942	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	35-40	3400	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3420907	A00947	7	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	30-35	4100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.1E+07
ERS3420908	A00947	4	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	30-35	4100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.5E+07
ERS3420909	A00947	21	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	30-35	4100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3420910	A00995	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.7E+07
ERS3420911	A00995	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.6E+07
ERS3420912	A00995	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.6E+07
ERS3420913	A01011	4	Vaginal	Vaginal	Neonatal	0	A	Postnatal	Female	35-40	3900	BF	Yes	NA	No	no	Yes	no	No	NA	low_Bacteroides	2.4E+07	1.9E+07
ERS3420914	A01011	Mother	Vaginal	Vaginal	Mother	0	A	NA	Female	35-40	3900	NA	NA	NA	No	no	Yes	no	NA	NA	NA	2.5E+07	2.1E+07
ERS3420915	A01011	7	Vaginal	Vaginal	Neonatal	0	A	Postnatal	Female	35-40	3900	BF	Yes	NA	No	no	Yes	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3420916	A01015	Infancy	Caesarean	Elective_CS	11.67	2	A	Postnatal	Female	30-35	3400	Mixed	Yes	NA	Yes	no	NA	no	No	NA	Low_Bacteroides	2.2E+07	2E+07
ERS3420917	A01015	Mother	Caesarean	Elective_CS	Mother	2	A	NA	Female	30-35	3400	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3420918	A01015	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	30-35	3400	Mixed	Yes	NA	Yes	no	NA	no	No	NA	Low_Bacteroides	1.7E+07	1.4E+07
ERS3420919	A01057	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	4100	NoBF	No	NA	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3420920	A01057	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	4100	NoBF	No	NA	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3420921	A01057	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	4100	Mixed	Yes	NA	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3420922	A01077	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	35-40	4200	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3420923	A01077	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	35-40	4200	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3420924	A01077	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	35-40	4200	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3420925	A01082	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	4400	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3420926	A01082	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	4400	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3420927	A01082	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	4400	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3420928	A01105	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3400	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3420929	A01105	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3400	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3420930	A01105	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3400	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.6E+07	1.4E+07
ERS3420931	A01107	Mother	Caesarean	Elective_CS	Mother	1	A	NA	Male	25-30	3700	NA	NA	NA	Yes	no	No	no	NA	NA	NA	2.3E+07	2E+07
ERS3420932	A01107	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	25-30	3700	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07

ERS3420933	A01107	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	25-30	3700	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3420934	A01107	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	25-30	3700	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3420935	A01162	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3700	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3420936	A01162	Infancy	Vaginal	Vaginal	11.53	1	A	Postnatal	Male	30-35	3700	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3420937	A01162	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3700	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3420938	A01166	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3200	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.7E+07	2.3E+07
ERS3420939	A01166	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3200	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3420940	A01166	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3200	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.9E+07	2.6E+07
ERS3420941	A01166	Infancy	Caesarean	Elective_CS	14.00	1	A	Postnatal	Female	35-40	3200	Mixed	Yes	No	Yes	no	No	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3420942	A01173	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	40-45	3900	BF	Yes	No	Yes	no	No	no	No	No	low_Bacteroides	2.9E+07	2.5E+07
ERS3420943	A01173	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	40-45	3900	BF	Yes	No	Yes	no	No	Yes	No	Yes	low_Bacteroides	2.4E+07	2.1E+07
ERS3420944	A01173	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	40-45	3900	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3420945	A01173	Infancy	Caesarean	Elective_CS	11.40	2	A	Postnatal	Female	40-45	3900	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3420946	A01174	4	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	30-35	3400	Mixed	Yes	No	Yes	no	No	no	NA	NA	low_Bacteroides	2.5E+07	2.3E+07
ERS3420947	A01174	7	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	30-35	3400	Mixed	Yes	No	Yes	no	No	no	NA	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3420948	A01174	21	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	30-35	3400	Mixed	Yes	No	Yes	no	No	no	NA	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3420949	A01176	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	40-45	3000	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3420950	A01176	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	40-45	3000	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3420951	A01176	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	40-45	3000	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3420952	A01225	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	30-35	4100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.2E+07	2.7E+07
ERS3420953	A01225	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	30-35	4100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	4E+07	3.5E+07
ERS3420954	A01225	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	30-35	4100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	4.1E+07	3.7E+07
ERS3420955	A01225	Infancy	Caesarean	Elective_CS	12.37	2	A	Postnatal	Female	30-35	4100	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3420956	A01301	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	30-35	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3420957	A01301	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	30-35	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.5E+07
ERS3420958	A01301	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	30-35	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.4E+07
ERS3420959	A01303	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3400	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3420960	A01303	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3400	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.5E+07
ERS3420961	A01303	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3400	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.6E+07
ERS3420962	A01303	Infancy	Caesarean	Elective_CS	10.77	1	A	Postnatal	Female	30-35	3400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3420963	A01305	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3420964	A01305	Infancy	Caesarean	Elective_CS	11.07	1	A	Postnatal	Female	35-40	3100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3420965	A01311	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	35-40	3900	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	4.1E+07	3.4E+07
ERS3420966	A01311	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	35-40	3900	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.4E+07
ERS3420967	A01431	7	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Female	30-35	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3420968	A01431	21	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Female	30-35	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3420969	A01431	Infancy	Caesarean	Emergency_	10.17	1	A	Postnatal	Female	30-35	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3420970	A01506	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	35-40	4100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3420971	A01506	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	35-40	4100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.5E+07	3.1E+07
ERS3420972	A01506	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	35-40	4100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.6E+07	3.3E+07
ERS3420973	A01506	Infancy	Caesarean	Elective_CS	9.63	2	A	Postnatal	Female	35-40	4100	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3420974	A01507	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3700	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.4E+07
ERS3420975	A01507	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3700	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2E+07
ERS3420976	A01507	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3700	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.2E+07	9113742
ERS3420977	A01507	Infancy	Caesarean	Elective_CS	9.70	1	A	Postnatal	Male	30-35	3700	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3420978	A01516	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	25-30	3600	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3420979	A01516	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	25-30	3600	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3420980	A01516	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	25-30	3600	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3420981	A01517	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3600	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3420982	A01517	Infancy	Caesarean	Elective_CS	10.17	1	A	Postnatal	Male	30-35	3600	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3420984	A01524	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	40-45	2900	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3420986	A01524	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	40-45	2900	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3420987	A01524	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	40-45	2900	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3420988	A01524	Infancy	Caesarean	Elective_CS	9.70	1	A	Postnatal	Female	40-45	2900	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3420989	A01563	Mother	Caesarean	Elective_CS	Mother	1	A	NA	Female	25-30	3500	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3420990	A01563	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	25-30	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3420991	A01563	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	25-30	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3420992	A01563	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	25-30	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3420993	A01569	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	3200	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3420994	A01569	Mother	Vaginal	Vaginal	Mother	1	A	NA	Male	25-30	3200	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.8E+07	2.5E+07
ERS3420995	A01580	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3300	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3420996	A01580	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3300	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3420997	A01580	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3300	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3420998	A01580	Infancy	Caesarean	Elective_CS	9.50	1	A	Postnatal	Female	30-35	3300	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3420999	A01582	7	Caesarean	Elective_CS	Neonatal	8	A	Postnatal	Male	35-40	1700	NA	NA	Yes	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.8E+07	2.5E+07
ERS3421000	A01582	21	Caesarean	Elective_CS	Neonatal	8	A	Postnatal	Male	35-40	1700	Mixed	Yes	Yes	Yes	no	NA	no	Yes	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421001	A01582	Infancy	Caesarean	Elective_CS	9.73	8	A	Postnatal	Male	35-40	1700	Mixed	Yes	Yes	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421002	A01583	21	Caesarean	Emergency_	Neonatal	2	A	Postnatal	Female	30-35	3500	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421003	A01583	4	Caesarean	Emergency_	Neonatal	2	A	Postnatal	Female	30-35	3500	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3421004	A01583	7	Caesarean	Emergency_	Neonatal	2	A	Postnatal	Female	30-35	3500	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421005	A01583	Infancy	Caesarean	Emergency_	9.40	2	A	Postnatal	Female	30-35	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.4E+07
ERS3421006	A01586	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	25-30	2400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421007	A01586	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	25-30	2400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421008	A01586	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	25-30	2400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421009	A01639	4	Caesarean	Elective_CS	Neonatal	5	A	Postnatal	Male	30-35	4400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3421010	A01639	21	Caesarean	Elective_CS	Neonatal	5	A	Postnatal	Male	30-35	4400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421011	A01639	7	Caesarean	Elective_CS	Neonatal	5	A	Postnatal	Male	30-35	4400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421012	A01646	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421013	A01646	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3421014	A01646	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3421015	A01646	Infancy	Caesarean	Elective_CS	10.50	1	A	Postnatal	Female	35-40	3100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3421016	A01647	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3500	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3421017	A01647	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3500	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421018	A01647	Infancy	Caesarean	Elective_CS	9.73	1	A	Postnatal	Female	30-35	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.3E+07
ERS3421019	A01653	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421020	A01653	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3421021	A01653	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3421022	A01653	Infancy	Caesarean	Elective_CS	9.07	1	A	Postnatal	Male	30-35	3100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.8E+07
ERS3421023	A01671	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	3800	NoBF	No	No	Yes	no	NA	no	NA	NA	low_Bacteroides	3.3E+07	2.8E+07
ERS3421024	A01671	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	3800	NoBF	No	No	Yes	no	NA	no	NA	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3421025	A01671	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	3800	NoBF	No	No	Yes	no	NA	no	NA	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421026	A01674	7	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	25-30	2700	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421027	A01674	21	Caesarean	Emergency_	Neonatal	1	A	Postnatal	Male	25-30	2700	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3421028	A01674	Infancy	Caesarean	Emergency_	9.50	1	A	Postnatal	Male	25-30	2700	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3421029	A01676	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3421030	A01676	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421031	A01676	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3421032	A01678	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	2600	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421033	A01678	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	2600	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3421034	A01678	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	25-30	2600	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07

ERS3421035	A01678	Infancy	Vaginal	Vaginal	9.10	1	A	Postnatal	Male	25-30	2600	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3421036	A01685	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	35-40	3000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3421037	A01685	Infancy	Caesarean	Elective_CS	NA	2	A	Postnatal	Male	35-40	3000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3421038	A01687	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	40-45	3800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.3E+07
ERS3421039	A01687	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	40-45	3800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.3E+07	2.6E+07
ERS3421040	A01687	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	40-45	3800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.7E+07	3.2E+07
ERS3421049	A01687	Infancy	Caesarean	Elective_CS	10.27	1	A	Postnatal	Female	40-45	3800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3421050	A01739	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.5E+07
ERS3421051	A01739	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	1.9E+07
ERS3421052	A01739	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.6E+07	2.8E+07
ERS3421053	A01739	Infancy	Caesarean	Elective_CS	8.70	1	A	Postnatal	Female	30-35	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421054	A01761	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	35-40	3000	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	2.1E+07
ERS3421055	A01761	Mother	Vaginal	Vaginal	Mother	1	A	NA	Male	35-40	3000	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.7E+07	2.4E+07
ERS3421056	A01761	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	35-40	3000	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.5E+07
ERS3421057	A01761	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	35-40	3000	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	1.7E+07
ERS3421058	A01761	Infancy	Vaginal	Vaginal	8.53	1	A	Postnatal	Male	35-40	3000	NA	NA	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.6E+07
ERS3421059	A01763	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421060	A01763	Mother	Vaginal	Vaginal	Mother	1	A	NA	Male	30-35	3600	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3421041	A01763	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421042	A01763	Infancy	Vaginal	Vaginal	8.63	1	A	Postnatal	Male	30-35	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.6E+07
ERS3421043	A01802	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	25-30	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421044	A01802	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	25-30	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.4E+07
ERS3421045	A01802	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	25-30	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.2E+07
ERS3421046	A01802	Infancy	Caesarean	Elective_CS	9.40	1	A	Postnatal	Female	25-30	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3421047	A01803	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	35-40	4300	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3421048	A01803	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	35-40	4300	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3421061	A01803	Mother	Caesarean	Elective_CS	Mother	2	A	NA	Male	35-40	4300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3421062	A01803	Infancy	Caesarean	Elective_CS	8.40	2	A	Postnatal	Male	35-40	4300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421063	A01805	21	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Female	30-35	3400	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.7E+07	1.2E+07
ERS3421064	A01805	4	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Female	30-35	3400	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.3E+07
ERS3421065	A01805	7	Vaginal	Vaginal	Neonatal	3	A	Postnatal	Female	30-35	3400	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.3E+07
ERS3421066	A01805	Mother	Vaginal	Vaginal	Mother	3	A	NA	Female	30-35	3400	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.7E+07	2.2E+07
ERS3421067	A01805	Infancy	Vaginal	Vaginal	8.40	3	A	Postnatal	Female	30-35	3400	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3421068	A01812	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Female	30-35	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.4E+07	1.2E+07
ERS3421069	A01812	Infancy	Vaginal	Vaginal	8.47	1	A	Postnatal	Female	30-35	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.3E+07
ERS3421070	A01812	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Female	30-35	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3421071	A01862	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	25-30	3800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3E+07	2.3E+07
ERS3421072	A01862	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	25-30	3800	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3421073	A01862	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	25-30	3800	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.4E+07
ERS3421074	A01866	21	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	35-40	4000	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.6E+07
ERS3421075	A01866	4	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	35-40	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.3E+07
ERS3421076	A01866	7	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	35-40	4000	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.4E+07
ERS3421077	A01910	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	2900	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421078	A01910	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	2900	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421079	A01910	Infancy	Vaginal	Vaginal	7.90	1	A	Postnatal	Male	30-35	2900	NA	NA	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3421080	A01921	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Female	30-35	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.5E+07
ERS3421081	A01921	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Female	30-35	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.5E+07
ERS3421082	A01921	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Female	30-35	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.7E+07
ERS3421083	A01921	Infancy	Vaginal	Vaginal	7.90	1	A	Postnatal	Female	30-35	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.5E+07
ERS3421084	A01938	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	30-35	3800	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3421085	A01938	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	30-35	3800	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.5E+07	3.2E+07
ERS3421086	A01938	Infancy	Caesarean	Elective_CS	7.77	2	A	Postnatal	Male	30-35	3800	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421087	A01939	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	4200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421088	A01939	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	4200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421089	A01939	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	4200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421090	A01939	Infancy	Caesarean	Elective_CS	10.00	1	A	Postnatal	Male	35-40	4200	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3421091	A01963	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	4200	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.3E+07
ERS3421092	A01963	Mother	Vaginal	Vaginal	Mother	1	A	NA	Male	30-35	4200	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2E+07
ERS3421093	A01963	Infancy	Vaginal	Vaginal	7.97	1	A	Postnatal	Male	30-35	4200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3421094	A01963	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	4200	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.4E+07
ERS3421095	A01966	21	Caesarean	Emergency_	Neonatal	5	A	SCBU	Female	30-35	3800	Mixed	Yes	Yes	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421096	A01966	4	Caesarean	Emergency_	Neonatal	5	A	SCBU	Female	30-35	3800	BF	Yes	Yes	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3421097	A01966	7	Caesarean	Emergency_	Neonatal	5	A	SCBU	Female	30-35	3800	Mixed	Yes	Yes	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3421098	A01966	Infancy	Caesarean	Emergency_	7.63	5	A	SCBU	Female	30-35	3800	Mixed	Yes	Yes	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.7E+07	2.3E+07
ERS3421099	A01970	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	40-45	3000	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3421100	A01970	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	40-45	3000	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3421101	A01970	Mother	Caesarean	Elective_CS	Mother	2	A	NA	Female	40-45	3000	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.1E+07	1.8E+07
ERS3421102	A01970	Infancy	Caesarean	Elective_CS	9.27	2	A	Postnatal	Female	40-45	3000	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.8E+07
ERS3421103	A02053	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3421104	A02053	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3421105	A02053	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421106	A02053	Infancy	Caesarean	Elective_CS	7.33	1	A	Postnatal	Male	30-35	3500	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421107	A02054	21	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	30-35	3400	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.1E+07
ERS3421108	A02054	4	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	30-35	3400	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.2E+07
ERS3421109	A02054	7	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	30-35	3400	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3421110	A02064	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421111	A02064	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421112	A02064	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	30-35	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421113	A02064	Mother	Caesarean	Elective_CS	Mother	1	A	NA	Male	30-35	3600	NA	NA	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421114	A02064	Infancy	Caesarean	Elective_CS	9.10	1	A	Postnatal	Male	30-35	3600	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3421115	A02080	7	Caesarean	Emergency_	Neonatal	2	A	Postnatal	Female	35-40	3600	Mixed	Yes	Yes	Yes	no	NA	Yes	No	Yes	low_Bacteroides	3E+07	2.7E+07
ERS3421116	A02080	Infancy	Caesarean	Emergency_	7.23	2	A	Postnatal	Female	35-40	3600	NA	NA	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3421117	A02080	Mother	Caesarean	Emergency_	Mother	2	A	NA	Female	35-40	3600	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3421118	A02096	4	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	25-30	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3421119	A02096	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	25-30	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.8E+07
ERS3421120	A02096	21	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Female	25-30	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.2E+07
ERS3421121	A02100	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	25-30	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.3E+07	1E+07
ERS3421122	A02100	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	25-30	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3421123	A02100	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	25-30	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.2E+07
ERS3421124	A02100	Infancy	Caesarean	Elective_CS	7.53	1	A	Postnatal	Male	25-30	3500	NA	NA	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421125	A02110	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421126	A02110	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3300	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421127	A02110	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3300	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3421128	A02110	Mother	Caesarean	Elective_CS	Mother	1	A	NA	Female	30-35	3300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2E+07	1.7E+07
ERS3421129	A02110	Infancy	Caesarean	Elective_CS	6.93	1	A	Postnatal	Female	30-35	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421130	A02133	21	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3500	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	1.9E+07	1.6E+07
ERS3421131	A02133	4	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421132	A02133	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	30-35	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.5E+07	2.1E+07
ERS3421133	A02138	Mother	Caesarean	Elective_CS	Mother	1	A	NA	Male	35-40	3600	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.2E+07	1.8E+07
ERS3421134	A02138	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	3600	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.5E+07

ERS3421135	A02138	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	3600	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421136	A02138	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	3600	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421137	A02138	Infancy	Caesarean	Elective_CS	7.10	1	A	Postnatal	Male	35-40	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3421138	A02146	21	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3500	NoBF	No	No	Yes	no	NA	no	No	Yes	low_Bacteroides	2.1E+07	1.8E+07
ERS3421139	A02146	4	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3500	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421140	A02146	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3500	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421141	A02146	Infancy	Caesarean	Elective_CS	7.17	1	A	Postnatal	Female	30-35	3500	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.5E+07
ERS3421142	A02177_T1	7	Caesarean	Elective_CS	Neonatal	6	A	Postnatal	Female	NA	2800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.7E+07	3.3E+07
ERS3421143	A02177_T1	Infancy	Caesarean	Elective_CS	6.47	6	A	Postnatal	Female	NA	2800	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.3E+07
ERS3421144	A02177_T2	7	Caesarean	Elective_CS	Neonatal	6	A	Postnatal	Female	NA	2800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421145	A02177_T2	Infancy	Caesarean	Elective_CS	6.53	6	A	Postnatal	Female	NA	2800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.4E+07
ERS3421146	A02193	7	Vaginal	Vaginal	Neonatal	0	A	NA	Male	35-40	3800	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	3.2E+07	2.7E+07
ERS3421147	A02193	Infancy	Vaginal	Vaginal	6.80	0	A	NA	Male	35-40	3800	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421148	A02193	Mother	Vaginal	Vaginal	Mother	0	A	NA	Male	35-40	3800	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3421149	A02222	Infancy	Caesarean	Elective_CS	6.33	1	A	Postnatal	Female	30-35	3100	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.4E+07	3.1E+07
ERS3421150	A02222	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	30-35	3100	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	1.6E+07	1.4E+07
ERS3421151	A02598	7	Caesarean	Elective_CS	Neonatal	3	A	Postnatal	Female	35-40	4000	Mixed	Yes	No	Yes	no	NA	Yes	No	Yes	low_Bacteroides	1.9E+07	1.7E+07
ERS3421152	A02598	Infancy	Caesarean	Elective_CS	7.13	3	A	Postnatal	Female	35-40	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421153	A02599	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	35-40	3900	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.2E+07	1E+07
ERS3421154	A02599	Infancy	Caesarean	Elective_CS	6.87	2	A	Postnatal	Male	35-40	3900	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3421155	A02600	Infancy	Caesarean	Elective_CS	7.03	2	A	Postnatal	Male	35-40	4200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421156	A02600	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	35-40	4200	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3421157	A02646	7	Caesarean	Elective_CS	Neonatal	2	A	Postnatal	Male	25-30	3400	BF	Yes	No	Yes	no	NA	Yes	No	Yes	low_Bacteroides	1.5E+07	1.3E+07
ERS3421158	A02646	Infancy	Caesarean	Elective_CS	6.80	2	A	Postnatal	Male	25-30	3400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3421159	A02767	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Female	25-30	2800	BF	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.6E+07	2.1E+07
ERS3421160	A02767	Mother	Vaginal	Vaginal	Mother	1	A	NA	Female	25-30	2800	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.7E+07	2.3E+07
ERS3421161	A02767	Infancy	Vaginal	Vaginal	6.30	1	A	Postnatal	Female	25-30	2800	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3421162	A02819	Mother	Caesarean	Elective_CS	Mother	1	A	NA	Male	35-40	3700	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.7E+07	2.3E+07
ERS3421163	A02819	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	3700	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.6E+07	2.2E+07
ERS3421164	A02819	Infancy	Caesarean	Elective_CS	5.87	1	A	Postnatal	Male	35-40	3700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421165	A02872	Mother	Caesarean	Elective_CS	Mother	1	A	NA	Male	35-40	4300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3421166	A02872	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Male	35-40	4300	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.6E+07	2.3E+07
ERS3421167	A02872	Infancy	Caesarean	Elective_CS	5.97	1	A	Postnatal	Male	35-40	4300	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3421168	A02886	7	Caesarean	Elective_CS	Neonatal	4	A	Postnatal	Female	30-35	3300	BF	Yes	No	Yes	no	NA	Yes	NA	Yes	low_Bacteroides	1.7E+07	1.6E+07
ERS3421169	A02886	Infancy	Caesarean	Elective_CS	5.90	4	A	Postnatal	Female	30-35	3300	NoBF	No	No	Yes	no	NA	no	NA	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421170	A02913	7	Caesarean	Elective_CS	Neonatal	3	A	NICU	Male	30-35	3300	NoBF	No	No	Yes	no	NA	no	Yes	No	low_Bacteroides	2.7E+07	2.3E+07
ERS3421171	A02913	Mother	Caesarean	Elective_CS	Mother	3	A	NA	Male	30-35	3300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.6E+07	2.2E+07
ERS3421172	A02913	Infancy	Caesarean	Elective_CS	6.03	3	A	NICU	Male	30-35	3300	NoBF	No	No	Yes	no	NA	no	Yes	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3421173	A03001	7	Caesarean	Elective_CS	Neonatal	1	A	Postnatal	Female	35-40	3000	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.1E+07	2E+07
ERS3421174	A03001	Infancy	Caesarean	Elective_CS	5.63	1	A	Postnatal	Female	35-40	3000	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3421175	A03026	Infancy	Vaginal	Vaginal	6.07	1	A	Postnatal	Male	20-25	3400	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3421176	A03026	7	Vaginal	Vaginal	Neonatal	1	A	Postnatal	Male	20-25	3400	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	1.6E+07	1.4E+07
ERS3421177	B00002	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3700	BF	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.4E+07	2.2E+07
ERS3421178	B00002	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3700	BF	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.3E+07	2E+07
ERS3421179	B00002	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3700	BF	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.2E+07
ERS3421180	B00004	Mother	Vaginal	Vaginal	Mother	3	B	NA	Male	40-45	3100	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.5E+07	2.2E+07
ERS3421181	B00004	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	40-45	3100	BF	Yes	Yes	NA	no	Yes	Yes	No	Yes	low_Bacteroides	2.1E+07	1.8E+07
ERS3421182	B00004	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	40-45	3100	Mixed	Yes	Yes	NA	no	Yes	no	No	Yes	low_Bacteroides	1.9E+07	1.7E+07
ERS3421183	B00008	21	Caesarean	Elective_CS	Neonatal	##	B	NICU	Male	20-25	700	Mixed	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421184	B00010	4	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Female	NA	3200	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.1E+07
ERS3421185	B00010	7	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Female	NA	3200	BF	Yes	No	Yes	no	NA	Yes	No	Yes	low_Bacteroides	2.4E+07	2.1E+07
ERS3421186	B00010	21	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Female	NA	3200	BF	Yes	No	Yes	no	NA	Yes	No	Yes	low_Bacteroides	2.5E+07	2.2E+07
ERS3421187	B00012	Mother	Vaginal	Vaginal	Mother	8	B	NA	Male	NA	2900	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	1.8E+07	1.6E+07
ERS3421188	B00012	4	Vaginal	Vaginal	Neonatal	8	B	Postnatal	Male	NA	2900	BF	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3421605	B00012	7	Vaginal	Vaginal	Neonatal	8	B	Postnatal	Male	NA	2900	BF	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.4E+07	2.3E+07
ERS3421606	B00013	4	Vaginal	Vaginal	Neonatal	0	B	Home	Female	NA	3200	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421607	B00013	7	Vaginal	Vaginal	Neonatal	0	B	Home	Female	NA	3200	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421608	B00013	21	Vaginal	Vaginal	Neonatal	0	B	Home	Female	NA	3200	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	2E+07
ERS3421609	B00016	7	Caesarean	Emergency	Neonatal	2	B	Postnatal	Female	NA	3300	Mixed	Yes	No	Yes	no	NA	Yes	No	Yes	low_Bacteroides	2.6E+07	2.4E+07
ERS3421610	B00016	4	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Female	NA	3300	Mixed	Yes	No	Yes	no	NA	no	No	Yes	low_Bacteroides	2.9E+07	2.7E+07
ERS3421611	B00016	21	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Female	NA	3300	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.9E+07
ERS3421612	B00017	4	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Male	NA	3200	BF	Yes	No	Yes	no	No	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3421613	B00017	21	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Male	NA	3200	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.5E+07	1.3E+07
ERS3421614	B00020	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	NA	3100	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421615	B00020	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	NA	3100	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3421616	B00020	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	NA	3100	Mixed	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	1.6E+07	1.4E+07
ERS3421617	B00027	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	NA	3600	NoBF	No	No	NA	no	Yes	no	No	Yes	low_Bacteroides	2.3E+07	2E+07
ERS3421618	B00027	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	NA	3600	NoBF	No	No	NA	no	Yes	no	No	Yes	low_Bacteroides	2.3E+07	2.1E+07
ERS3421619	B00036	4	Vaginal	Vaginal	Neonatal	NA	B	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.2E+07	2.1E+07
ERS3421620	B00036	7	Vaginal	Vaginal	Neonatal	NA	B	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3421621	B00036	21	Vaginal	Vaginal	Neonatal	NA	B	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3421622	B00040	Mother	Vaginal	Vaginal	Mother	1	B	NA	Female	NA	3200	NA	NA	NA	NA	no	NA	no	NA	NA	NA	1.8E+07	1.6E+07
ERS3421623	B00040	4	Vaginal	Vaginal	Neonatal	1	B	Home	Female	NA	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2.1E+07
ERS3421624	B00046	Mother	Vaginal	Vaginal	Mother	3	B	NA	Female	NA	3400	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.5E+07	2.3E+07
ERS3421625	B00046	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	NA	3400	BF	Yes	No	NA	no	Yes	Yes	No	Yes	low_Bacteroides	2.1E+07	1.9E+07
ERS3421626	B00046	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	NA	3400	BF	Yes	No	NA	no	Yes	Yes	No	Yes	low_Bacteroides	2.2E+07	1.9E+07
ERS3421627	B00046	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	NA	3400	BF	Yes	No	NA	no	Yes	Yes	No	Yes	low_Bacteroides	1.9E+07	1.7E+07
ERS3421628	B00052	7	Vaginal	Vaginal	Neonatal	0	B	Home	Male	NA	3700	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	1.7E+07	1.5E+07
ERS3421629	B00052	21	Vaginal	Vaginal	Neonatal	0	B	Home	Male	NA	3700	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	1.9E+07	1.7E+07
ERS3421630	B00053	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	NA	2900	BF	Yes	No	Yes	no	NA	Yes	No	Yes	low_Bacteroides	3.1E+07	2.9E+07
ERS3421631	B00053	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	NA	2900	BF	Yes	No	Yes	no	NA	no	No	Yes	low_Bacteroides	2.8E+07	2.5E+07
ERS3421632	B00053	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	NA	2900	BF	Yes	No	Yes	no	NA	Yes	No	Yes	low_Bacteroides	2.4E+07	2.1E+07
ERS3421633	B00057	4	Vaginal	Vaginal	Neonatal	1	B	Home	Male	NA	3800	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.2E+07	1.8E+07
ERS3421634	B00057	7	Vaginal	Vaginal	Neonatal	1	B	Home	Male	NA	3800	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.7E+07
ERS3421635	B00064	4	Vaginal	Vaginal	Neonatal	1	B	NICU	Female	NA	3300	NoBF	No	No	NA	no	NA	no	No	No	low_Bacteroides	2.4E+07	2E+07
ERS3421636	B00064	7	Vaginal	Vaginal	Neonatal	1	B	NICU	Female	NA	3300	NoBF	No	No	NA	no	NA	no	No	No	low_Bacteroides	2.4E+07	2.1E+07
ERS3421637	B00064	21	Vaginal	Vaginal	Neonatal	1	B	NICU	Female	NA	3300	NoBF	No	No	NA	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3421638	B00070	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	NA	4500	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	2E+07
ERS3421639	B00070	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	NA	4500	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.7E+07
ERS3421640	B00070	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	NA	4500	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.8E+07
ERS3421641	B00071	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	NA	2600	BF	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.4E+07	2.1E+07
ERS3421642	B00071	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	NA	2600	BF	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3421643	B00071	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	NA	2600	BF	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3421644	B00075	Mother	Caesarean	Emergency_	Mother	2	B	NA	Male	20-25	3200	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.1E+07	1.9E+07
ERS3421645	B00075	4	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Male	20-25	3200	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3421646	B00075	7	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Male	20-25	3200	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421647	B00075	21	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Male	20-25	3200	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3421648	B00076	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421649	B00076	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421650	B00077	4	Caesarean	Elective_CS	Neonatal	0	B	NICU	Male	25-30	2800	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.5E+07

ERS3421651	B00077	7	Caesarean	Elective_CS	Neonatal	0	B	NICU	Male	25-30	2800	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421652	B00077	21	Caesarean	Elective_CS	Neonatal	0	B	NICU	Male	25-30	2800	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421653	B00085	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3500	BF	Yes	Yes	Yes	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421654	B00085	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3500	BF	Yes	Yes	Yes	no	NA	no	No	NA	normal_Bacteroides	2.7E+07	2.4E+07
ERS3421655	B00088	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	25-30	2900	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421656	B00088	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	25-30	2900	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421657	B00090	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	30-35	3000	BF	Yes	Yes	NA	no	NA	Yes	No	Yes	low_Bacteroides	2.1E+07	1.8E+07
ERS3421658	B00090	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	30-35	3000	BF	Yes	Yes	NA	no	NA	Yes	No	Yes	low_Bacteroides	2.5E+07	2.1E+07
ERS3421659	B00090	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	30-35	3000	BF	Yes	Yes	NA	no	NA	no	No	Yes	low_Bacteroides	2.4E+07	2.1E+07
ERS3421660	B00092	21	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	25-30	3000	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	2.2E+07	1.9E+07
ERS3421661	B00092	4	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	25-30	3000	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	2.4E+07	2.1E+07
ERS3421662	B00092	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	25-30	3000	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.8E+07
ERS3421663	B00096	7	Caesarean	Emergency	Neonatal	3	B	Postnatal	Male	35-40	3500	NoBF	No	Yes	Yes	no	No	Yes	No	Yes	low_Bacteroides	2.3E+07	2E+07
ERS3421664	B00096	21	Caesarean	Emergency	Neonatal	3	B	Postnatal	Male	35-40	3500	Mixed	Yes	Yes	Yes	no	No	no	No	No	low_Bacteroides	2.3E+07	2E+07
ERS3421665	B00097	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	20-25	2500	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	2E+07
ERS3421666	B00097	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	20-25	2500	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	2.1E+07
ERS3421667	B00097	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	20-25	2500	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	2E+07
ERS3421668	B00099	Mother	Vaginal	Vaginal	Mother	3	B	NA	Male	35-40	4500	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.6E+07	2.3E+07
ERS3421669	B00099	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	35-40	4500	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3421670	B00099	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	35-40	4500	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3421671	B00100	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3100	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2.7E+07	2.4E+07
ERS3421672	B00100	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3100	BF	Yes	No	NA	no	NA	no	No	Yes	low_Bacteroides	2.4E+07	2E+07
ERS3421673	B00101	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	2800	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.4E+07	2.2E+07
ERS3421674	B00101	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	2800	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421675	B00101	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	2800	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	2E+07
ERS3421676	B00111	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.5E+07
ERS3421677	B00111	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3421678	B00112	4	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	30-35	2500	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.6E+07	2.2E+07
ERS3421679	B00112	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	30-35	2500	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.7E+07	2.2E+07
ERS3421680	B00116	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3421681	B00116	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3421682	B00119	4	Vaginal	Vaginal	Neonatal	0	B	Home	Male	25-30	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421683	B00119	7	Vaginal	Vaginal	Neonatal	0	B	Home	Male	25-30	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3421684	B00119	21	Vaginal	Vaginal	Neonatal	0	B	Home	Male	25-30	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.6E+07
ERS3421685	B00120	4	Caesarean	Emergency	Neonatal	6	B	Postnatal	Male	20-25	3500	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	3E+07	2.6E+07
ERS3421686	B00120	7	Caesarean	Emergency	Neonatal	6	B	Postnatal	Male	20-25	3500	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421687	B00129	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3700	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.2E+07
ERS3421688	B00129	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3700	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.2E+07
ERS3421689	B00136	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3000	Mixed	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.8E+07
ERS3421690	B00136	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3000	Mixed	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.4E+07	2.2E+07
ERS3421691	B00136	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3000	Mixed	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.2E+07	1.9E+07
ERS3421692	B00139	Mother	Caesarean	Elective_CS	Mother	3	B	NA	Female	30-35	3300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.5E+07	2.2E+07
ERS3421693	B00139	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	30-35	3300	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	2.2E+07	2E+07
ERS3421694	B00139	21	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	30-35	3300	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3421695	B00140	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3500	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2E+07	1.8E+07
ERS3421696	B00140	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3500	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3421697	B00140	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3500	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.8E+07
ERS3421698	B00145	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	35-40	2300	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3421699	B00145	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	35-40	2300	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.8E+07
ERS3421700	B00145	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	35-40	2300	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.4E+07	2E+07
ERS3421701	B00146	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3500	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.5E+07	2.2E+07
ERS3421702	B00146	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3500	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.2E+07	2E+07
ERS3421703	B00146	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3500	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.7E+07	2.4E+07
ERS3421704	B00149	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3300	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.8E+07	2.5E+07
ERS3421705	B00149	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3300	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.4E+07	2.2E+07
ERS3421706	B00149	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3300	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.2E+07
ERS3421707	B00153	4	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Male	30-35	5100	BF	Yes	Yes	NA	no	NA	Yes	No	Yes	low_Bacteroides	1.9E+07	1.6E+07
ERS3421708	B00153	7	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Male	30-35	5100	BF	Yes	Yes	NA	no	NA	no	No	Yes	low_Bacteroides	1.9E+07	1.6E+07
ERS3421709	B00153	21	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Male	30-35	5100	BF	Yes	Yes	NA	no	NA	no	No	Yes	low_Bacteroides	1.8E+07	1.5E+07
ERS3421710	B00157_T3	4	Caesarean	Elective_CS	Neonatal	14	B	NICU	Male	NA	2000	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.8E+07	2.5E+07
ERS3421715	B00157_T2	4	Caesarean	Elective_CS	Neonatal	14	B	NICU	Male	NA	2000	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.3E+07
ERS3421716	B00157_T3	7	Caesarean	Elective_CS	Neonatal	14	B	NICU	Male	NA	2000	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.2E+07
ERS3421717	B00157_T2	7	Caesarean	Elective_CS	Neonatal	14	B	NICU	Male	NA	2000	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.3E+07	2E+07
ERS3421718	B00157_T2	21	Caesarean	Elective_CS	Neonatal	14	B	NICU	Male	NA	2000	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.8E+07
ERS3421719	B00157_T3	21	Caesarean	Elective_CS	Neonatal	14	B	NICU	Male	NA	2000	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.6E+07
ERS3421720	B00174	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421721	B00174	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3421722	B00174	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3421723	B00175	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	2700	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3421724	B00175	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	2700	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3421725	B00176	4	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Male	35-40	3400	Mixed	Yes	No	NA	no	Yes	no	No	NA	normal_Bacteroides	2E+07	1.6E+07
ERS3421726	B00176	21	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Male	35-40	3400	Mixed	Yes	No	NA	no	Yes	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3421727	B00178	4	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	35-40	2800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421728	B00178	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	35-40	2800	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3421711	B00178	21	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	35-40	2800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3421712	B00203_T2	7	Caesarean	Elective_CS	Neonatal	5	B	Postnatal	Male	NA	2300	Mixed	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	1.7E+07	1.3E+07
ERS3421713	B00203_T1	21	Caesarean	Elective_CS	Neonatal	5	B	Postnatal	Male	NA	2300	Mixed	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2E+07	1.6E+07
ERS3421714	B00203_T2	21	Caesarean	Elective_CS	Neonatal	5	B	Postnatal	Male	NA	2300	Mixed	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3421729	B00203_T1	7	Caesarean	Elective_CS	Neonatal	5	B	Postnatal	Male	NA	2300	Mixed	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.4E+07	1.9E+07
ERS3421730	B00203_T2	4	Caesarean	Elective_CS	Neonatal	5	B	Postnatal	Male	NA	2300	Mixed	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421731	B00220	Mother	Vaginal	Vaginal	Mother	0	B	NA	Male	30-35	3700	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.1E+07	1.9E+07
ERS3421732	B00220	4	Vaginal	Vaginal	Neonatal	0	B	Home	Male	30-35	3700	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3421733	B00224	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	2000	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3421734	B00224	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	2000	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421735	B00224	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	2000	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.3E+07
ERS3421736	B00235	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	40-45	4000	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.4E+07	1.3E+07
ERS3421737	B00235	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	40-45	4000	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.4E+07
ERS3421738	B00235	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	40-45	4000	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.4E+07
ERS3421739	B00236	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	25-30	3700	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.6E+07
ERS3421740	B00236	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	25-30	3700	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.6E+07
ERS3421741	B00236	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	25-30	3700	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.7E+07
ERS3421742	B00238	7	Caesarean	Emergency	Neonatal	4	B	Postnatal	Female	30-35	3500	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3421743	B00238	Mother	Caesarean	Emergency	Mother	4	B	NA	Female	30-35	3500	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3421744	B00243	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	3100	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3421745	B00243	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	3100	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3421746	B00243	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	3100	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3421747	B00252	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	3700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.6E+07
ERS3421748	B00252	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	3700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3E+07	2.7E+07
ERS3421749	B00252	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	3700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.4E+07
ERS3421750	B00268	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	2600	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.2E+07

ERS3421751	B00268	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	2600	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	1.9E+07
ERS3421752	B00268	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	2600	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421753	B00272	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	4600	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3421754	B00272	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	4600	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421755	B00272	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	4600	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.6E+07
ERS3421756	B00507	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	40-45	4300	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.7E+07	1.3E+07
ERS3421757	B00507	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	40-45	4300	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421758	B00507	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	40-45	4300	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421759	B00509	4	Vaginal	Vaginal	Neonatal	0	B	Home	Female	40-45	2500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3421760	B00509	Infancy	Vaginal	Vaginal	11.70	0	B	Home	Female	40-45	2500	Mixed	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.4E+07	2E+07
ERS3421761	B00518	4	Caesarean	Elective_CS	Neonatal	8	B	Postnatal	Male	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.4E+07
ERS3421762	B00518	7	Caesarean	Elective_CS	Neonatal	8	B	Postnatal	Male	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3421763	B00518	21	Caesarean	Elective_CS	Neonatal	8	B	Postnatal	Male	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.7E+07
ERS3421764	B00537	7	Vaginal	Vaginal	Neonatal	10	B	NICU	Male	40-45	3100	BF	Yes	Yes	No	no	No	no	Yes	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3421765	B00537	21	Vaginal	Vaginal	Neonatal	10	B	NICU	Male	40-45	3100	BF	Yes	Yes	No	no	No	no	Yes	NA	low_Bacteroides	2.4E+07	1.9E+07
ERS3421766	B00537	4	Vaginal	Vaginal	Neonatal	10	B	NICU	Male	40-45	3100	BF	Yes	Yes	No	no	No	no	Yes	NA	low_Bacteroides	1.7E+07	1.3E+07
ERS3421767	B00537	Mother	Vaginal	Vaginal	Mother	10	B	NA	Male	40-45	3100	NA	NA	NA	No	no	No	no	Yes	NA	NA	2.5E+07	2.1E+07
ERS3421768	B00550	21	Caesarean	Elective_CS	Neonatal	7	B	Postnatal	Female	30-35	4400	Mixed	Yes	Yes	Yes	no	No	no	Yes	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3421769	B00550	Mother	Caesarean	Elective_CS	Mother	7	B	NA	Female	30-35	4400	NA	NA	NA	Yes	no	No	no	Yes	NA	NA	2.4E+07	2E+07
ERS3421770	B00553	7	Caesarean	Emergency	Neonatal	4	B	Postnatal	Male	40-45	3100	NoBF	No	No	Yes	Yes	No	no	Yes	NA	low_Bacteroides	2E+07	1.6E+07
ERS3421771	B00553	4	Caesarean	Emergency	Neonatal	4	B	Postnatal	Male	40-45	3100	Mixed	Yes	No	Yes	Yes	No	no	Yes	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3421772	B00553	21	Caesarean	Emergency	Neonatal	4	B	Postnatal	Male	40-45	3100	NoBF	No	No	Yes	Yes	No	no	Yes	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3421773	B00560	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	3100	BF	Yes	No	No	no	No	no	No	NA	normal_Bacteroides	2.1E+07	1.6E+07
ERS3421774	B00560	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	3100	BF	Yes	No	No	no	No	no	No	NA	normal_Bacteroides	2.1E+07	1.7E+07
ERS3421775	B00560	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	3100	BF	Yes	No	No	no	No	no	No	NA	normal_Bacteroides	1.9E+07	1.6E+07
ERS3421776	B00562_T2	4	Caesarean	Elective_CS	Neonatal	15	B	Postnatal	Female	NA	2200	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.5E+07	1.9E+07
ERS3421777	B00562_T1	7	Caesarean	Elective_CS	Neonatal	15	B	Postnatal	Female	NA	2200	NoBF	No	No	Yes	no	No	no	No	NA	low_Bacteroides	2.4E+07	1.9E+07
ERS3421778	B00562_T2	7	Caesarean	Elective_CS	Neonatal	15	B	Postnatal	Female	NA	2200	NoBF	No	No	Yes	no	No	no	No	NA	low_Bacteroides	2E+07	1.5E+07
ERS3421779	B00562_T1	21	Caesarean	Elective_CS	Neonatal	15	B	Postnatal	Female	NA	2200	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.3E+07	1.7E+07
ERS3421780	B00562_T2	21	Caesarean	Elective_CS	Neonatal	15	B	Postnatal	Female	NA	2200	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.5E+07	1.9E+07
ERS3421781	B00916	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.4E+07	1.8E+07
ERS3421782	B00916	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.6E+07
ERS3421783	B00916	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3421784	B00917	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.7E+07	1.2E+07
ERS3421785	B00917	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.5E+07
ERS3421786	B00917	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.6E+07
ERS3421787	B00922	7	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Male	25-30	4100	Mixed	Yes	Yes	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.4E+07	1.9E+07
ERS3421788	B00922	Mother	Vaginal	Vaginal	Mother	4	B	NA	Male	25-30	4100	NA	NA	NA	NA	no	Yes	no	Yes	NA	NA	2.3E+07	2E+07
ERS3421789	B01021	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.2E+07
ERS3421790	B01021	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3421791	B01021	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3421792	B01022	7	Vaginal	Vaginal	Neonatal	6	B	NICU	Female	30-35	4000	BF	Yes	Yes	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3421793	B01022	Mother	Vaginal	Vaginal	Mother	6	B	NA	Female	30-35	4000	NA	NA	NA	NA	no	NA	no	Yes	NA	NA	2.3E+07	1.9E+07
ERS3421794	B01027	Mother	Vaginal	Vaginal	Mother	0	B	NA	Male	35-40	3600	NA	NA	NA	No	no	No	no	NA	NA	NA	2.5E+07	2E+07
ERS3421795	B01027	7	Vaginal	Vaginal	Neonatal	0	B	Home	Male	35-40	3600	Mixed	Yes	No	No	no	No	no	No	NA	normal_Bacteroides	2.6E+07	2.2E+07
ERS3421796	B01034	Mother	Caesarean	Elective_CS	Mother	2	B	NA	Male	25-30	3500	NA	NA	NA	Yes	Yes	No	no	NA	NA	NA	2.3E+07	1.9E+07
ERS3421797	B01034	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	25-30	3500	Mixed	Yes	No	Yes	Yes	No	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421798	B01039	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Female	20-25	3000	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3421799	B01039	Mother	Vaginal	Vaginal	Mother	0	B	NA	Female	20-25	3000	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2E+07
ERS3421800	B01042	Mother	Caesarean	Elective_CS	Mother	2	B	NA	Male	30-35	3400	NA	NA	NA	Yes	no	No	no	NA	NA	NA	2.3E+07	1.8E+07
ERS3421801	B01042	10	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3400	BF	Yes	Yes	Yes	no	No	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3421802	B01042	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3400	BF	Yes	Yes	Yes	no	No	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3421803	B01089	Mother	Caesarean	Elective_CS	Mother	2	B	NA	Female	35-40	3900	NA	NA	NA	Yes	no	No	no	NA	NA	NA	2.2E+07	1.8E+07
ERS3421804	B01089	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3900	Mixed	Yes	Yes	Yes	no	No	no	No	NA	low_Bacteroides	2.7E+07	2.3E+07
ERS3421805	B01089	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3900	Mixed	Yes	Yes	Yes	no	No	no	No	NA	low_Bacteroides	2.8E+07	2.4E+07
ERS3421806	B01089	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3900	Mixed	Yes	Yes	Yes	no	No	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3421807	B01128	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	30-35	3200	BF	Yes	Yes	No	no	No	no	No	NA	normal_Bacteroides	1.4E+07	1.3E+07
ERS3421808	B01128	Mother	Vaginal	Vaginal	Mother	2	B	NA	Male	30-35	3200	NA	NA	NA	No	no	No	no	NA	NA	NA	1.7E+07	1.6E+07
ERS3421809	B01190	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	2900	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421810	B01190	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	2900	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.9E+07	2.6E+07
ERS3421811	B01190	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	2900	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	3E+07	2.6E+07
ERS3421812	B01190	Infancy	Caesarean	Elective_CS	12.40	2	B	Postnatal	Male	35-40	2900	NA	NA	No	Yes	no	No	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421813	B01194	4	Vaginal	Vaginal	Neonatal	1	B	Home	Male	25-30	3300	NoBF	No	No	No	no	No	no	No	NA	normal_Bacteroides	1.9E+07	1.6E+07
ERS3421814	B01194	Mother	Vaginal	Vaginal	Mother	1	B	NA	Male	25-30	3300	NA	NA	NA	No	no	No	no	NA	NA	NA	2.1E+07	1.9E+07
ERS3421815	B01194	7	Vaginal	Vaginal	Neonatal	1	B	Home	Male	25-30	3300	NoBF	No	No	No	no	No	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3421816	B01194	21	Vaginal	Vaginal	Neonatal	1	B	Home	Male	25-30	3300	NoBF	No	No	No	no	No	no	No	NA	normal_Bacteroides	2.5E+07	2.1E+07
ERS3421817	B01194	Infancy	Vaginal	Vaginal	12.53	1	B	Home	Male	25-30	3300	NA	NA	No	No	no	No	no	No	NA	normal_Bacteroides	1.7E+07	1.6E+07
ERS3421818	B01196	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3600	NoBF	No	Yes	No	no	No	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3421819	B01196	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3600	NoBF	No	Yes	No	no	No	no	No	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3421820	B01196	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3600	NoBF	No	Yes	No	no	No	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3421821	B01218	Infancy	Vaginal	Vaginal	13.27	1	B	Postnatal	Male	35-40	3600	NA	NA	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.7E+07
ERS3421822	B01218	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3600	NA	NA	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.7E+07
ERS3421823	B01234	7	Vaginal	Vaginal	Neonatal	8	B	Postnatal	Male	30-35	3900	BF	Yes	Yes	NA	no	NA	no	Yes	NA	low_Bacteroides	1.8E+07	1.7E+07
ERS3421824	B01234	Mother	Vaginal	Vaginal	Mother	8	B	NA	Male	30-35	3900	NA	NA	NA	NA	no	NA	no	Yes	NA	NA	1.5E+07	1.5E+07
ERS3421825	B01234	Infancy	Vaginal	Vaginal	12.57	8	B	Postnatal	Male	30-35	3900	NA	NA	Yes	NA	no	NA	no	Yes	NA	low_Bacteroides	1.7E+07	1.6E+07
ERS3421826	B01235	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3100	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.5E+07	2.1E+07
ERS3421827	B01235	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3100	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.5E+07	2.1E+07
ERS3421828	B01235	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3100	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.5E+07	2.2E+07
ERS3421829	B01236	4	Caesarean	Emergency	Neonatal	2	B	Postnatal	Male	25-30	3500	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3421830	B01236	7	Caesarean	Emergency	Neonatal	2	B	Postnatal	Male	25-30	3500	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421831	B01236	21	Caesarean	Emergency	Neonatal	2	B	Postnatal	Male	25-30	3500	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3421832	B01236	Infancy	Caesarean	Emergency	12.27	2	B	Postnatal	Male	25-30	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3421833	B01242	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	40-45	3900	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3421834	B01242	Infancy	Caesarean	Elective_CS	11.50	3	B	Postnatal	Male	40-45	3900	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3421835	B01247	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	35-40	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.4E+07	1.3E+07
ERS3421836	B01247	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	35-40	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.4E+07	1.3E+07
ERS3421837	B01247	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	35-40	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.6E+07
ERS3421838	B01256	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	30-35	2700	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421839	B01256	Infancy	Caesarean	Elective_CS	12.20	3	B	Postnatal	Male	30-35	2700	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421840	B01261	Mother	Vaginal	Vaginal	Mother	2	B	NA	Female	25-30	3800	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.5E+07	2.2E+07
ERS3421841	B01261	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	25-30	3800	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.6E+07
ERS3421842	B01261	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	25-30	3800	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3421843	B01261	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	25-30	3800	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421844	B01265	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	35-40	3500	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421845	B01265	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	35-40	3500	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421846	B01265	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	35-40	3500	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421847	B01265	Infancy	Vaginal	Vaginal	11.93	1	B	Postnatal	Female	35-40	3500	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3421848	B01277	Mother	Vaginal	Vaginal	Mother	0	B	NA	Female	20-25	3600	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.6E+07	2.2E+07
ERS3421849	B01277	4	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Female	20-25	3600	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	2E+07
ERS3421850	B01277	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Female	20-25	3600	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07

ERS3421851	B01277	21	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Female	20-25	3600	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3421852	B01278	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3E+07	2.6E+07
ERS3421853	B01278	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3400	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3421854	B01278	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3400	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421855	B01278	Infancy	Caesarean	Elective_CS	12.03	2	B	Postnatal	Female	35-40	3400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3421856	B01284	21	Vaginal	Vaginal	Neonatal	0	B	Home	Male	30-35	4200	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.4E+07	1.3E+07
ERS3421857	B01284	4	Vaginal	Vaginal	Neonatal	0	B	Home	Male	30-35	4200	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.4E+07
ERS3421858	B01284	7	Vaginal	Vaginal	Neonatal	0	B	Home	Male	30-35	4200	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.7E+07	1.4E+07
ERS3421859	B01284	Infancy	Vaginal	Vaginal	11.23	0	B	Home	Male	30-35	4200	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3421860	B01299	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3400	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.3E+07	1.2E+07
ERS3421861	B01299	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3400	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.3E+07	1.2E+07
ERS3421862	B01299	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3400	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3421863	B01299	Infancy	Vaginal	Vaginal	11.70	1	B	Postnatal	Male	35-40	3400	NA	NA	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.4E+07	2.1E+07
ERS3421864	B01339	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	40-45	3700	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.4E+07
ERS3421865	B01339	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	40-45	3700	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.3E+07
ERS3421866	B01339	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	40-45	3700	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3421867	B01339	Infancy	Vaginal	Vaginal	11.50	1	B	Postnatal	Male	40-45	3700	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421868	B01340	Mother	Vaginal	Vaginal	Mother	1	B	NA	Male	20-25	3000	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.6E+07	2.3E+07
ERS3421869	B01340	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	20-25	3000	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421870	B01340	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	20-25	3000	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421871	B01340	14	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	20-25	3000	NoBF	No	No	NA	no	NA		No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421872	B01364	Mother	Vaginal	Vaginal	Mother	2	B	NA	Male	30-35	3100	NA	NA	NA	NA	no	NA	no	NA	NA	NA	1.7E+07	1.5E+07
ERS3421873	B01364	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	30-35	3100	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421874	B01364	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	30-35	3100	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421875	B01364	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	30-35	3100	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.4E+07
ERS3421876	B01364	Infancy	Vaginal	Vaginal	11.43	2	B	Postnatal	Male	30-35	3100	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.7E+07	2.3E+07
ERS3421877	B01365	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	4100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.3E+07
ERS3421878	B01365	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	4100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.4E+07
ERS3421879	B01365	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	4100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3421880	B01365	Infancy	Caesarean	Elective_CS	11.37	2	B	Postnatal	Male	35-40	4100	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421881	B01368	7	Vaginal	Vaginal	Neonatal	0	B	Home	Male	25-30	3000	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.4E+07
ERS3421882	B01368	Mother	Vaginal	Vaginal	Mother	0	B	NA	Male	25-30	3000	NA	NA	NA	NA	no	NA	no	NA	NA	NA	1.6E+07	1.4E+07
ERS3421883	B01372_T1	7	Caesarean	Emergency_	Neonatal	7	B	Postnatal	Male	NA	2000	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.6E+07
ERS3421884	B01372_T2	7	Caesarean	Emergency_	Neonatal	7	B	Postnatal	Male	NA	2000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.1E+07	2.8E+07
ERS3421885	B01372_T1	Infancy	Caesarean	Emergency_	11.57	7	B	Postnatal	Male	NA	2000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3421886	B01372_T2	Infancy	Caesarean	Emergency_	NA	7	B	Postnatal	Male	NA	2000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421887	B01373	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	20-25	4500	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.5E+07
ERS3421888	B01373	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	20-25	4500	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3421889	B01373	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	20-25	4500	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.5E+07
ERS3421890	B01373	Infancy	Vaginal	Vaginal	12.43	1	B	Postnatal	Female	20-25	4500	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.1E+07	1.9E+07
ERS3421891	B01374	Infancy	Caesarean	Elective_CS	12.00	2	B	Postnatal	Female	25-30	3200	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3421892	B01374	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3200	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3421893	B01375	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	25-30	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.3E+07
ERS3421894	B01375	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	25-30	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.4E+07	1.3E+07
ERS3421895	B01375	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	25-30	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.4E+07	1.3E+07
ERS3421896	B01406	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	25-30	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421897	B01406	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	25-30	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421898	B01406	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	25-30	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3421899	B01406	Infancy	Vaginal	Vaginal	11.23	3	B	Postnatal	Female	25-30	3500	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.4E+07	2.1E+07
ERS3421900	B01408	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3400	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421901	B01408	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3400	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.4E+07
ERS3421902	B01408	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3400	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.4E+07
ERS3421903	B01408	Mother	Vaginal	Vaginal	Mother	1	B	NA	Male	30-35	3400	NA	NA	NA	NA	no	NA	no	NA	NA	NA	1.5E+07	1.4E+07
ERS3421904	B01408	Infancy	Vaginal	Vaginal	14.27	1	B	Postnatal	Male	30-35	3400	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3421905	B01409	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	3000	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	3E+07	2.6E+07
ERS3421906	B01409	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	3000	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.4E+07
ERS3421907	B01409	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	3000	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.7E+07	1.3E+07
ERS3421908	B01409	Mother	Vaginal	Vaginal	Mother	1	B	NA	Male	25-30	3000	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.7E+07	2.3E+07
ERS3421909	B01413	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	30-35	4400	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.4E+07
ERS3421910	B01413	21	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	30-35	4400	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.6E+07	1.5E+07
ERS3421911	B01413	4	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	30-35	4400	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.4E+07	1.3E+07
ERS3421912	B01415	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	3300	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421913	B01415	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	3300	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421914	B01415	Infancy	Caesarean	Elective_CS	11.10	2	B	Postnatal	Male	35-40	3300	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3421915	B01416	7	Vaginal	Vaginal	Neonatal	0	B	Home	Female	30-35	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.4E+07
ERS3421916	B01416	Infancy	Vaginal	Vaginal	11.17	0	B	Home	Female	30-35	3500	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3421917	B01417	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	30-35	3400	NoBF	No	Yes	NA	no	NA	no	NA	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3421918	B01417	Infancy	Vaginal	Vaginal	11.10	2	B	Postnatal	Female	30-35	3400	Mixed	Yes	Yes	NA	no	NA	no	NA	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421919	B01417	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	30-35	3400	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421920	B01421	Infancy	Vaginal	Vaginal	11.33	1	B	Postnatal	Female	30-35	2900	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.6E+07
ERS3421921	B01421	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	2900	NA	NA	No	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3421922	B01423	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3600	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	3.2E+07	2.7E+07
ERS3421923	B01423	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3600	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.8E+07	2.2E+07
ERS3421924	B01423	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3600	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3421925	B01423	Infancy	Vaginal	Vaginal	11.13	1	B	Postnatal	Female	30-35	3600	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421926	B01424	21	Caesarean	Emergency_	Neonatal	5	B	Postnatal	Female	40-45	2400	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.6E+07	3.2E+07
ERS3421927	B01424	7	Caesarean	Emergency_	Neonatal	5	B	Postnatal	Female	40-45	2400	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.7E+07
ERS3421928	B01424	4	Caesarean	Emergency_	Neonatal	5	B	Postnatal	Female	40-45	2400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	2E+07
ERS3421929	B01438	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	20-25	3500	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421930	B01438	Infancy	Vaginal	Vaginal	11.10	2	B	Postnatal	Female	20-25	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.7E+07	1.5E+07
ERS3421931	B01450_T2	21	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Female	NA	2300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3421932	B01450_T1	4	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Female	NA	2300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3421933	B01450_T2	4	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Female	NA	2300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421934	B01450_T1	7	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Female	NA	2300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3421935	B01450_T2	7	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Female	NA	2300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421936	B01450_T1	21	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Female	NA	2300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3421937	B01450_T1	Infancy	Caesarean	Emergency_	10.93	3	B	Postnatal	Female	NA	2300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3421938	B01450_T2	Infancy	Caesarean	Emergency_	10.93	3	B	Postnatal	Female	NA	2300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3421939	B01471	7	Caesarean	Elective_CS	Neonatal	5	B	Postnatal	Female	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3421940	B01471	Mother	Caesarean	Elective_CS	Mother	5	B	NA	Female	35-40	3100	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3421941	B01471	21	Caesarean	Elective_CS	Neonatal	5	B	Postnatal	Female	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421942	B01472	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3200	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421943	B01472	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3200	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.1E+07	2.8E+07
ERS3421944	B01472	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3200	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3421945	B01472	Infancy	Caesarean	Elective_CS	10.97	2	B	Postnatal	Male	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2E+07	1.6E+07
ERS3421946	B01497	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	20-25	3300	BF	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421947	B01497	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	20-25	3300	BF	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.1E+07	1.9E+07
ERS3421948	B01497	Infancy	Vaginal	Vaginal	10.73	1	B	Postnatal	Male	20-25	3300	Mixed	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.5E+07	2.2E+07
ERS3421949	B01536	7	Caesarean	Emergency_	Neonatal	1	B	Postnatal	Male	35-40	4300	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3421950	B01536	Infancy	Caesarean	Emergency_	10.47	1	B	Postnatal	Male	35-40	4300	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07

ERS3421951	B01539	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3800	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421952	B01539	Infancy	Vaginal	Vaginal	10.43	1	B	Postnatal	Female	30-35	3800	NoBF	No	No	NA	no	NA	no	No	NA	low_Bacteroides	3.2E+07	2.9E+07
ERS3421953	B01540	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3000	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421954	B01540	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3000	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3421955	B01540	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3000	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3421956	B01540	Infancy	Vaginal	Vaginal	10.50	1	B	Postnatal	Female	30-35	3000	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3421957	B01543	21	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	20-25	4100	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421958	B01543	4	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	20-25	4100	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3421959	B01543	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	20-25	4100	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421960	B01543	Infancy	Vaginal	Vaginal	10.40	0	B	Postnatal	Male	20-25	4100	NA	NA	No	NA	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421961	B01548	21	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Male	30-35	3900	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421962	B01548	Infancy	Caesarean	Emergency_	10.43	3	B	Postnatal	Male	30-35	3900	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421963	B01572	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	20-25	4000	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3421964	B01572	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	20-25	4000	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.6E+07
ERS3421965	B01572	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	20-25	4000	NA	NA	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3421966	B01572	Infancy	Vaginal	Vaginal	10.43	2	B	Postnatal	Female	20-25	4000	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3421967	B01574	Infancy	Caesarean	Emergency_	10.47	1	B	Postnatal	Male	35-40	4000	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3421968	B01574	4	Caesarean	Emergency_	Neonatal	1	B	Postnatal	Male	35-40	4000	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3421969	B01600	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3421978	B01600	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3421979	B01600	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.3E+07
ERS3421980	B01600	Infancy	Caesarean	Elective_CS	10.37	2	B	Postnatal	Female	30-35	3100	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3421981	B01610	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	20-25	3100	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3421982	B01610	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	20-25	3100	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421983	B01610	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	20-25	3100	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421984	B01616	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	20-25	4500	NoBF	No	No	NA	no	NA	no	Yes	NA	low_Bacteroides	2E+07	1.6E+07
ERS3421985	B01616	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	20-25	4500	NoBF	No	No	NA	no	NA	no	Yes	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3421986	B01616	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	20-25	4500	NoBF	No	No	NA	no	NA	no	Yes	NA	low_Bacteroides	2.7E+07	2.3E+07
ERS3421987	B01616	Infancy	Vaginal	Vaginal	10.27	3	B	Postnatal	Male	20-25	4500	NA	NA	No	NA	no	NA	no	Yes	No	low_Bacteroides	2E+07	1.6E+07
ERS3421988	B01626	7	Vaginal	Vaginal	Neonatal	7	B	Postnatal	Female	40-45	2200	NA	NA	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421970	B01626	Infancy	Vaginal	Vaginal	10.60	7	B	Postnatal	Female	40-45	2200	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.2E+07	1.9E+07
ERS3421971	B01627	7	Vaginal	Vaginal	Neonatal	5	B	Postnatal	Female	30-35	2200	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3421972	B01627	Infancy	Vaginal	Vaginal	10.33	5	B	Postnatal	Female	30-35	2200	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3421973	B01633	21	Vaginal	Vaginal	Neonatal	0	B	Home	Male	35-40	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3421974	B01633	4	Vaginal	Vaginal	Neonatal	0	B	Home	Male	35-40	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3421975	B01633	7	Vaginal	Vaginal	Neonatal	0	B	Home	Male	35-40	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3421976	B01635	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	30-35	4700	NA	NA	No	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421977	B01635	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	30-35	4700	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3421989	B01635	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	30-35	4700	NA	NA	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3421990	B01664	21	Vaginal	Vaginal	Neonatal	0	B	Home	Female	30-35	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3421991	B01664	4	Vaginal	Vaginal	Neonatal	0	B	Home	Female	30-35	2900	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	3.2E+07	2.9E+07
ERS3421992	B01664	7	Vaginal	Vaginal	Neonatal	0	B	Home	Female	30-35	2900	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.6E+07
ERS3421993	B01664	Infancy	Vaginal	Vaginal	10.03	0	B	Home	Female	30-35	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3421994	B01668	7	Vaginal	Vaginal	Neonatal	0	B	NA	Male	30-35	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.2E+07	2E+07
ERS3421995	B01668	Infancy	Vaginal	Vaginal	10.23	0	B	NA	Male	30-35	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3421996	B01670	7	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Female	35-40	2600	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3421997	B01670	Infancy	Vaginal	Vaginal	10.07	4	B	Postnatal	Female	35-40	2600	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3421998	B01710	7	Vaginal	Vaginal	Neonatal	0	B	NICU	Male	40-45	3800	NoBF	No	No	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.5E+07	2.2E+07
ERS3421999	B01710	21	Vaginal	Vaginal	Neonatal	0	B	NICU	Male	40-45	3800	NoBF	No	No	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.4E+07	2.1E+07
ERS3422000	B01710	Infancy	Vaginal	Vaginal	9.77	0	B	NICU	Male	40-45	3800	NA	NA	No	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422001	B01712	4	Caesarean	Elective_CS	Neonatal	3	B	NICU	Male	40-45	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.2E+07	2.8E+07
ERS3422002	B01712	7	Caesarean	Elective_CS	Neonatal	3	B	NICU	Male	40-45	3300	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422003	B01712	21	Caesarean	Elective_CS	Neonatal	3	B	NICU	Male	40-45	3300	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422004	B01712	Infancy	Caesarean	Elective_CS	9.73	3	B	NICU	Male	40-45	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422005	B01714	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	30-35	3200	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422006	B01714	Infancy	Vaginal	Vaginal	9.77	2	B	Postnatal	Female	30-35	3200	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422007	B01714	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	30-35	3200	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3422008	B01716	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	3300	NA	NA	No	NA	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.6E+07
ERS3422009	B01716	Mother	Vaginal	Vaginal	Mother	2	B	NA	Female	35-40	3300	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.5E+07	2.2E+07
ERS3422010	B01716	Infancy	Vaginal	Vaginal	9.80	2	B	Postnatal	Female	35-40	3300	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422011	B01719	4	Vaginal	Vaginal	Neonatal	1	B	Home	Male	30-35	3100	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.1E+07
ERS3422012	B01719	7	Vaginal	Vaginal	Neonatal	1	B	Home	Male	30-35	3100	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.5E+07
ERS3422013	B01719	Mother	Vaginal	Vaginal	Mother	1	B	NA	Male	30-35	3100	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.6E+07	2.2E+07
ERS3422014	B01719	21	Vaginal	Vaginal	Neonatal	1	B	Home	Male	30-35	3100	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422015	B01719	Infancy	Vaginal	Vaginal	9.90	1	B	Home	Male	30-35	3100	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.6E+07	1.5E+07
ERS3422016	B01725	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3422017	B01725	Infancy	Caesarean	Elective_CS	10.00	2	B	Postnatal	Male	30-35	4000	NA	NA	No	Yes	no	NA	no	No	No	low_Bacteroides	2.6E+07	2.3E+07
ERS3422018	B01729	Infancy	Vaginal	Vaginal	10.07	0	B	Postnatal	Male	35-40	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422019	B01729	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	35-40	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422020	B01771	Mother	Vaginal	Vaginal	Mother	1	B	NA	Female	35-40	4200	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.2E+07	2E+07
ERS3422021	B01771	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	35-40	4200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422022	B01771	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	35-40	4200	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2.1E+07
ERS3422023	B01771	Infancy	Vaginal	Vaginal	9.93	1	B	Postnatal	Female	35-40	4200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422024	B01772	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3200	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422025	B01772	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3200	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422026	B01772	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3200	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422027	B01772	Mother	Caesarean	Elective_CS	Mother	2	B	NA	Female	30-35	3200	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.6E+07	2.3E+07
ERS3422028	B01772	Infancy	Caesarean	Elective_CS	9.50	2	B	Postnatal	Female	30-35	3200	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422029	B01773	Infancy	Vaginal	Vaginal	9.77	1	B	Home	Male	30-35	4400	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422030	B01773	7	Vaginal	Vaginal	Neonatal	1	B	Home	Male	30-35	4400	NA	NA	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422031	B01775	21	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Female	30-35	4000	NoBF	No	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3422032	B01775	4	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Female	30-35	4000	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422033	B01775	7	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Female	30-35	4000	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422034	B01775	Infancy	Vaginal	Vaginal	9.50	4	B	Postnatal	Female	30-35	4000	NA	NA	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422035	B01782	4	Vaginal	Vaginal	Neonatal	0	B	Home	Female	25-30	3100	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.5E+07
ERS3422036	B01782	7	Vaginal	Vaginal	Neonatal	0	B	Home	Female	25-30	3100	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.7E+07
ERS3422037	B01782	21	Vaginal	Vaginal	Neonatal	0	B	Home	Female	25-30	3100	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.4E+07
ERS3422038	B01782	Infancy	Vaginal	Vaginal	9.60	0	B	Home	Female	25-30	3100	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422039	B01784	7	Caesarean	Emergency_	Neonatal	7	B	NICU	Female	25-30	3700	BF	Yes	No	Yes	no	No	no	Yes	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422040	B01784	21	Caesarean	Emergency_	Neonatal	7	B	NICU	Female	25-30	3700	BF	Yes	No	Yes	no	No	no	Yes	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422041	B01784	Infancy	Caesarean	Emergency_	10.77	7	B	NICU	Female	25-30	3700	Mixed	Yes	No	Yes	no	No	no	Yes	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3422042	B01786	7	Vaginal	Vaginal	Neonatal	4	B	NICU	Male	30-35	3900	NA	NA	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422043	B01786	Infancy	Vaginal	Vaginal	9.77	4	B	NICU	Male	30-35	3900	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422044	B01787_T1	Infancy	Vaginal	Vaginal	9.57	30	B	NICU	Male	NA	1700	Mixed	Yes	No	No	no	Yes	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422045	B01787_T2	7	Vaginal	Vaginal	Neonatal	30	B	NICU	Male	NA	1700	Mixed	Yes	No	No	no	Yes	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3422046	B01787_T2	Infancy	Vaginal	Vaginal	9.57	30	B	NICU	Male	NA	1700	Mixed	Yes	No	No	no	Yes	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422047	B01787_T1	7	Vaginal	Vaginal	Neonatal	30	B	NICU	Male	NA	1700	Mixed	Yes	No	No	no	Yes	no	No	NA	normal_Bacteroides	2.3E+07	2.1E+07
ERS3422048	B01789	7	Caesarean	Elective_CS	Neonatal	1	B	Postnatal	Female	30-35	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422049	B01789	Infancy	Caesarean	Elective_CS	9.63	1	B	Postnatal	Female	30-35	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422050	B01791	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	20-25	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07

ERS3422051	B01791	Infancy	Vaginal	Vaginal	9.37	0	B	Postnatal	Male	20-25	2900	NA	NA	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422052	B01791	4	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	20-25	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422053	B01796	Infancy	Caesarean	Elective_CS	9.57	3	B	Postnatal	Female	35-40	3200	NoBF	No	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.7E+07
ERS3422054	B01796	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	35-40	3200	NA	NA	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422055	B01797	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422056	B01797	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3500	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422057	B01797	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	35-40	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422058	B01797	Infancy	Vaginal	Vaginal	9.47	1	B	Postnatal	Male	35-40	3500	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3422059	B01798	4	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	30-35	3100	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422060	B01798	Infancy	Vaginal	Vaginal	9.33	0	B	Postnatal	Male	30-35	3100	Mixed	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.4E+07	2E+07
ERS3422061	B01799	Infancy	Vaginal	Vaginal	9.37	0	B	Home	Female	25-30	3800	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422062	B01799	7	Vaginal	Vaginal	Neonatal	0	B	Home	Female	25-30	3800	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3422063	B01800	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	3700	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3422064	B01800	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	3700	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422065	B01800	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	3700	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422066	B01813	Infancy	Vaginal	Vaginal	9.27	2	B	Postnatal	Female	35-40	4000	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422067	B01813	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	4000	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.7E+07	2.4E+07
ERS3422068	B01829	21	Vaginal	Vaginal	Neonatal	1	B	Home	Male	30-35	3500	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422069	B01829	4	Vaginal	Vaginal	Neonatal	1	B	Home	Male	30-35	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.9E+07	2.6E+07
ERS3422070	B01829	7	Vaginal	Vaginal	Neonatal	1	B	Home	Male	30-35	3500	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.5E+07	2.1E+07
ERS3422071	B01829	Infancy	Vaginal	Vaginal	11.47	1	B	Home	Male	30-35	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422072	B01830	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	30-35	4000	NA	NA	No	NA	no	NA	no	Yes	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422073	B01830	Infancy	Vaginal	Vaginal	11.17	2	B	Postnatal	Male	30-35	4000	Mixed	Yes	No	NA	no	NA	no	Yes	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422074	B01847	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422075	B01847	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422076	B01847	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.4E+07
ERS3422077	B01847	Infancy	Vaginal	Vaginal	9.40	1	B	Postnatal	Female	25-30	3200	NoBF	No	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422078	B01848	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	2700	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422079	B01848	Infancy	Caesarean	Elective_CS	10.27	2	B	Postnatal	Female	25-30	2700	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422080	B01851	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	25-30	2700	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422081	B01851	Infancy	Vaginal	Vaginal	9.10	3	B	Postnatal	Female	25-30	2700	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422082	B01890	21	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	35-40	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422083	B01890	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	35-40	3500	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.2E+07	2.8E+07
ERS3422084	B01890	Infancy	Caesarean	Elective_CS	7.77	3	B	Postnatal	Female	35-40	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422085	B01891	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	30-35	4000	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422086	B01891	Mother	Vaginal	Vaginal	Mother	2	B	NA	Male	30-35	4000	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.2E+07	1.8E+07
ERS3422087	B01891	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	30-35	4000	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422088	B01892	4	Caesarean	Emergency	Neonatal	2	B	Postnatal	Male	35-40	3700	NoBF	No	No	Yes	no	NA		No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422089	B01892	7	Caesarean	Emergency	Neonatal	2	B	Postnatal	Male	35-40	3700	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3422090	B01892	Infancy	Caesarean	Emergency	8.97	2	B	Postnatal	Male	35-40	3700	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422091	B01906	7	Caesarean	Emergency	Neonatal	6	B	NICU	Male	30-35	4500	Mixed	Yes	No	Yes	no	No	no	Yes	NA	low_Bacteroides	2.8E+07	2.4E+07
ERS3422092	B01906	21	Caesarean	Emergency	Neonatal	6	B	NICU	Male	30-35	4500	Mixed	Yes	No	Yes	no	No	no	Yes	NA	low_Bacteroides	2.9E+07	2.5E+07
ERS3422093	B01906	Infancy	Caesarean	Emergency	10.40	6	B	NICU	Male	30-35	4500	Mixed	Yes	No	Yes	no	No	no	Yes	No	low_Bacteroides	2.1E+07	1.9E+07
ERS3422094	B01944	7	Vaginal	Vaginal	Neonatal	6	B	Postnatal	Male	35-40	3700	BF	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422095	B01944	Infancy	Vaginal	Vaginal	8.93	6	B	Postnatal	Male	35-40	3700	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422096	B01947	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	40-45	2600	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3E+07	2.5E+07
ERS3422097	B01947	Mother	Caesarean	Elective_CS	Mother	3	B	NA	Male	40-45	2600	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.4E+07	1.9E+07
ERS3422098	B01948	7	Vaginal	Vaginal	Neonatal	0	B	Home	Female	25-30	2100	NoBF	No	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.1E+07
ERS3422099	B01948	Mother	Vaginal	Vaginal	Mother	0	B	NA	Female	25-30	2100	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.6E+07	2.1E+07
ERS3422100	B01948	Infancy	Vaginal	Vaginal	8.80	0	B	Home	Female	25-30	2100	NA	NA	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422101	B01954	21	Caesarean	Elective_CS	Neonatal	1	B	Postnatal	NA	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422102	B01954	4	Caesarean	Elective_CS	Neonatal	1	B	Postnatal	NA	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3422103	B01954	7	Caesarean	Elective_CS	Neonatal	1	B	Postnatal	NA	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422104	B01954	Infancy	Caesarean	Elective_CS	10.67	1	B	Postnatal	NA	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3422105	B01956	21	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	30-35	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3422106	B01956	4	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	30-35	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3422107	B01956	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	30-35	3200	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	3.2E+07	2.6E+07
ERS3422108	B01956	Infancy	Vaginal	Vaginal	8.87	0	B	Postnatal	Male	30-35	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422109	B02002	Infancy	Caesarean	Elective_CS	9.37	3	B	Postnatal	Female	35-40	3300	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422110	B02002	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	35-40	3300	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422111	B02005	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	25-30	3200	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3422112	B02005	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	25-30	3200	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422113	B02005	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	25-30	3200	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422114	B02005	Mother	Caesarean	Elective_CS	Mother	2	B	NA	Male	25-30	3200	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.1E+07	1.7E+07
ERS3422115	B02029	Infancy	Caesarean	Elective_CS	8.70	2	B	Postnatal	Female	25-30	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.2E+07	1.8E+07
ERS3422116	B02029	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.5E+07
ERS3422117	B02069	Infancy	Caesarean	Elective_CS	8.57	4	B	Postnatal	Male	30-35	3800	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422118	B02069	7	Caesarean	Elective_CS	Neonatal	4	B	Postnatal	Male	30-35	3800	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3422119	B02075	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	30-35	4300	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3422120	B02075	Mother	Vaginal	Vaginal	Mother	0	B	NA	Male	30-35	4300	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.3E+07	1.9E+07
ERS3422121	B02098	21	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	35-40	2800	BF	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422122	B02098	4	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	35-40	2800	BF	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422123	B02098	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	35-40	2800	BF	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3422124	B02098	Mother	Caesarean	Elective_CS	Mother	3	B	NA	Male	35-40	2800	NA	NA	NA	Yes	no	NA	no	Yes	NA	NA	2.4E+07	2.1E+07
ERS3422125	B02103	21	Caesarean	Emergency	Neonatal	3	B	Postnatal	Male	30-35	3600	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.3E+07	2.9E+07
ERS3422126	B02103	Infancy	Caesarean	Emergency	7.70	3	B	Postnatal	Male	30-35	3600	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3422127	B02106	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	3200	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422128	B02106	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	3200	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3422129	B02106	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	35-40	3200	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3422130	B02106	Infancy	Caesarean	Elective_CS	7.67	2	B	Postnatal	Male	35-40	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422131	B02109	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3422132	B02109	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3422133	B02109	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3422134	B02118	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3100	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422135	B02118	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3100	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	2.1E+07
ERS3422136	B02118	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3100	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422137	B02118	Infancy	Vaginal	Vaginal	7.67	1	B	Postnatal	Male	30-35	3100	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422138	B02147	21	Vaginal	Vaginal	Neonatal	3	B	NICU	Female	30-35	4500	BF	Yes	No	NA	no	NA	no	Yes	No	normal_Bacteroides	2E+07	1.7E+07
ERS3422139	B02147	4	Vaginal	Vaginal	Neonatal	3	B	NICU	Female	30-35	4500	BF	Yes	No	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422140	B02147	7	Vaginal	Vaginal	Neonatal	3	B	NICU	Female	30-35	4500	BF	Yes	No	NA	no	NA	no	Yes	No	normal_Bacteroides	2.1E+07	1.7E+07
ERS3422141	B02147	Infancy	Vaginal	Vaginal	7.43	3	B	NICU	Female	30-35	4500	Mixed	Yes	No	NA	no	NA	no	Yes	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422142	B02153	21	Caesarean	Emergency	Neonatal	2	B	Postnatal	Male	30-35	3600	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	3.4E+07	2.9E+07
ERS3422143	B02153	Infancy	Caesarean	Emergency	7.43	2	B	Postnatal	Male	30-35	3600	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3422144	B02156	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3000	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422145	B02156	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3000	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	2.1E+07
ERS3422146	B02156	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3000	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.5E+07	2.1E+07
ERS3422147	B02156	Infancy	Vaginal	Vaginal	7.47	1	B	Postnatal	Male	30-35	3000	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.6E+07
ERS3422148	B02159	7	Caesarean	Emergency	Neonatal	7	B	Postnatal	Female	25-30	4400	Mixed	Yes	No	Yes	no	No	no	Yes	NA	low_Bacteroides	1.5E+07	1.2E+07
ERS3422149	B02159	21	Caesarean	Emergency	Neonatal	7	B	Postnatal	Female	25-30	4400	Mixed	Yes	No	Yes	no	No	no	Yes	Yes	low_Bacteroides	2.2E+07	1.9E+07
ERS3422150	B02159	Mother	Caesarean	Emergency	Mother	7	B	NA	Female	25-30	4400	NA	NA	NA	Yes	no	No	no	Yes	NA	NA	2.4E+07	2.1E+07

ERS3422151	B02159	Infancy	Caesarean	Emergency_	7.37	7	B	Postnatal	Female	25-30	4400	Mixed	Yes	No	Yes	no	No	no	Yes	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3422152	B02165	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3800	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.3E+07	2.9E+07
ERS3422153	B02165	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3800	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.6E+07
ERS3422154	B02165	Infancy	Caesarean	Elective_CS	7.43	2	B	Postnatal	Female	30-35	3800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422155	B02166	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	4300	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.4E+07	2.9E+07
ERS3422156	B02166	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	4300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.4E+07
ERS3422157	B02166	Infancy	Caesarean	Elective_CS	7.43	2	B	Postnatal	Female	40-45	4300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422158	B02200	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Female	30-35	4300	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422159	B02200	Infancy	Vaginal	Vaginal	6.70	0	B	Postnatal	Female	30-35	4300	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422160	B02209	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	4100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.5E+07
ERS3422161	B02209	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	4100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422162	B02209	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	4100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422163	B02211	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	30-35	3700	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422164	B02211	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	30-35	3700	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	2E+07
ERS3422165	B02211	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	30-35	3700	Mixed	Yes	Yes	NA	no	NA	Yes	No	Yes	normal_Bacteroides	2E+07	1.7E+07
ERS3422166	B02211	Infancy	Vaginal	Vaginal	7.13	3	B	Postnatal	Female	30-35	3700	Mixed	Yes	Yes	NA	no	NA	no	No	Yes	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422167	B02215	21	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Male	45-50	2400	NoBF	No	No	Yes	no	No	Yes	No	Yes	low_Bacteroides	2.1E+07	1.8E+07
ERS3422168	B02215	4	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Male	45-50	2400	NoBF	No	No	Yes	no	No	Yes	No	Yes	low_Bacteroides	2.3E+07	1.9E+07
ERS3422169	B02215	7	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Male	45-50	2400	NoBF	No	No	Yes	no	No	Yes	No	Yes	low_Bacteroides	1.5E+07	1.3E+07
ERS3422170	B02216	21	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	40-45	3800	NoBF	No	No	Yes	no	NA	no	Yes	No	low_Bacteroides	2.2E+07	1.9E+07
ERS3422171	B02216	4	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	40-45	3800	NoBF	No	No	Yes	no	NA	no	Yes	No	low_Bacteroides	2.2E+07	1.9E+07
ERS3422172	B02216	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	40-45	3800	NoBF	No	No	Yes	no	NA	no	Yes	No	low_Bacteroides	1.9E+07	1.6E+07
ERS3422173	B02216	Infancy	Caesarean	Elective_CS	6.87	3	B	Postnatal	Female	40-45	3800	NoBF	No	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422174	B02218	Infancy	Vaginal	Vaginal	7.43	6	B	Postnatal	Female	20-25	3100	NA	NA	No	NA	no	NA	no	Yes	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422175	B02218	7	Vaginal	Vaginal	Neonatal	6	B	Postnatal	Female	20-25	3100	BF	Yes	No	NA	no	NA	no	Yes	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422176	B02243	Mother	Vaginal	Vaginal	Mother	3	B	NA	Female	20-25	2700	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.7E+07	2.3E+07
ERS3422177	B02243	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	20-25	2700	Mixed	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.3E+07	1.9E+07
ERS3422178	B02243	Infancy	Vaginal	Vaginal	7.23	3	B	Postnatal	Female	20-25	2700	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422179	B02247	4	Caesarean	Emergency_	Neonatal	4	B	Postnatal	Male	35-40	4300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3422180	B02247	7	Caesarean	Emergency_	Neonatal	4	B	Postnatal	Male	35-40	4300	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.4E+07	2.1E+07
ERS3422181	B02247	21	Caesarean	Emergency_	Neonatal	4	B	Postnatal	Male	35-40	4300	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.2E+07	1.9E+07
ERS3422182	B02247	Infancy	Caesarean	Emergency_	7.30	4	B	Postnatal	Male	35-40	4300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.3E+07
ERS3422183	B02248	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3700	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.7E+07	2.4E+07
ERS3422184	B02248	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3700	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422185	B02248	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	30-35	3700	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422186	B02248	Infancy	Caesarean	Elective_CS	7.07	2	B	Postnatal	Male	30-35	3700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422187	B02249	4	Vaginal	Vaginal	Neonatal	2	B	NICU	Male	30-35	3800	BF	Yes	Yes	NA	no	NA	no	Yes	Yes	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422188	B02249	21	Vaginal	Vaginal	Neonatal	2	B	NICU	Male	30-35	3800	BF	Yes	Yes	NA	no	NA	no	Yes	No	normal_Bacteroides	2.1E+07	1.7E+07
ERS3422189	B02249	7	Vaginal	Vaginal	Neonatal	2	B	NICU	Male	30-35	3800	BF	Yes	Yes	NA	no	NA	no	Yes	No	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422190	B02249	Mother	Vaginal	Vaginal	Mother	2	B	NA	Male	30-35	3800	NA	NA	NA	NA	no	NA	no	Yes	NA	NA	2.8E+07	2.3E+07
ERS3422191	B02254	7	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Male	30-35	3600	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3422192	B02254	Infancy	Caesarean	Emergency_	7.80	2	B	Postnatal	Male	30-35	3600	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422193	B02255	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	45-50	3500	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.3E+07
ERS3422194	B02255	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	45-50	3500	NoBF	No	No	Yes	no	NA	Yes	No	Yes	low_Bacteroides	2.8E+07	2.5E+07
ERS3422195	B02255	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	45-50	3500	NoBF	No	No	Yes	no	NA	no	No	Yes	low_Bacteroides	1.6E+07	1.3E+07
ERS3422196	B02255	Infancy	Caesarean	Elective_CS	7.07	2	B	Postnatal	Female	45-50	3500	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422197	B02257	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	2500	NA	NA	No	NA	no	Yes	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3422198	B02257	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	2500	NA	NA	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3422199	B02257	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	2500	NA	NA	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422200	B02257	Infancy	Vaginal	Vaginal	6.97	1	B	Postnatal	Male	25-30	2500	Mixed	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422201	B02258	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3900	BF	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.7E+07
ERS3422202	B02258	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3900	Mixed	Yes	No	NA	no	NA	Yes	No	Yes	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422203	B02258	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3900	BF	Yes	No	NA	no	NA	no	No	Yes	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422204	B02258	Infancy	Vaginal	Vaginal	7.07	1	B	Postnatal	Female	30-35	3900	Mixed	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.4E+07	2E+07
ERS3422205	B02263	7	Vaginal	Vaginal	Neonatal	6	B	NICU	Female	30-35	NA	NA	NA	No	NA	no	NA	no	Yes	NA	low_Bacteroides	3.1E+07	2.7E+07
ERS3422206	B02263	Mother	Vaginal	Vaginal	Mother	6	B	NA	Female	30-35	NA	NA	NA	NA	NA	no	NA	no	Yes	NA	NA	2.3E+07	1.9E+07
ERS3422207	B02263	Infancy	Vaginal	Vaginal	7.27	6	B	NICU	Female	30-35	NA	Mixed	Yes	No	NA	no	NA	no	Yes	NA	low_Bacteroides	2E+07	1.6E+07
ERS3422208	B02270	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3600	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3422209	B02270	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3600	BF	Yes	Yes	Yes	no	NA	no	No	Yes	low_Bacteroides	2.2E+07	1.8E+07
ERS3422210	B02270	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	25-30	3600	BF	Yes	Yes	Yes	no	NA	Yes	No	Yes	low_Bacteroides	2.5E+07	2.2E+07
ERS3422211	B02273	21	Vaginal	Vaginal	Neonatal	1	B	Home	Female	30-35	2700	BF	Yes	Yes	NA	no	NA	no	No	Yes	normal_Bacteroides	2.3E+07	1.7E+07
ERS3422212	B02273	4	Vaginal	Vaginal	Neonatal	1	B	Home	Female	30-35	2700	BF	Yes	Yes	NA	no	NA	Yes	No	Yes	normal_Bacteroides	3.3E+07	2.6E+07
ERS3422213	B02273	Mother	Vaginal	Vaginal	Mother	1	B	NA	Female	30-35	2700	NA	NA	NA	NA	no	NA	no	NA	NA	NA	3.2E+07	2.6E+07
ERS3422214	B02273	7	Vaginal	Vaginal	Neonatal	1	B	Home	Female	30-35	2700	BF	Yes	Yes	NA	no	NA	Yes	No	Yes	normal_Bacteroides	2.8E+07	2.2E+07
ERS3422215	B02273	Infancy	Vaginal	Vaginal	6.80	1	B	Home	Female	30-35	2700	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422216	B02274	7	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Female	30-35	3100	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3422217	B02274	Infancy	Caesarean	Emergency_	9.63	2	B	Postnatal	Female	30-35	3100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422218	B02286	4	Vaginal	Vaginal	Neonatal	0	B	Home	Male	35-40	3700	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.5E+07	2E+07
ERS3422219	B02286	Mother	Vaginal	Vaginal	Mother	0	B	NA	Male	35-40	3700	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.5E+07	2.1E+07
ERS3422220	B02287	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	25-30	3600	BF	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422221	B02287	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	25-30	3600	BF	Yes	No	NA	no	Yes	no	No	Yes	low_Bacteroides	3E+07	2.7E+07
ERS3422222	B02287	Infancy	Vaginal	Vaginal	6.97	3	B	Postnatal	Female	25-30	3600	Mixed	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422223	B02306	7	Vaginal	Vaginal	Neonatal	3	B	Home	Female	30-35	4000	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2.1E+07	2E+07
ERS3422224	B02306	Infancy	Vaginal	Vaginal	6.13	3	B	Home	Female	30-35	4000	NA	NA	No	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.3E+07
ERS3422225	B02313	21	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Male	30-35	3300	BF	Yes	No	Yes	no	No	no	No	Yes	low_Bacteroides	2.4E+07	2E+07
ERS3422226	B02313	7	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Male	30-35	3300	BF	Yes	No	Yes	no	No	Yes	No	Yes	low_Bacteroides	2.6E+07	2.3E+07
ERS3422227	B02313	Infancy	Caesarean	Emergency_	6.83	2	B	Postnatal	Male	30-35	3300	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422228	B02315	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	4100	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	2.8E+07	2.5E+07
ERS3422229	B02315	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	4100	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.2E+07
ERS3422230	B02315	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	40-45	4100	NoBF	No	No	Yes	no	NA	no	No	Yes	low_Bacteroides	2.2E+07	1.9E+07
ERS3422231	B02316	7	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Female	35-40	3200	Mixed	Yes	Yes	Yes	no	NA	no	No	Yes	low_Bacteroides	2.1E+07	1.9E+07
ERS3422232	B02316	Infancy	Caesarean	Emergency_	6.97	2	B	Postnatal	Female	35-40	3200	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422252	B02317	4	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Female	35-40	3300	Mixed	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.8E+07
ERS3422253	B02317	21	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Female	35-40	3300	Mixed	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.4E+07	2E+07
ERS3422254	B02317	7	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Female	35-40	3300	Mixed	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.2E+07	1.9E+07
ERS3422255	B02317	Infancy	Vaginal	Vaginal	6.83	4	B	Postnatal	Female	35-40	3300	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3422233	B02320_T1	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	NA	3200	NA	NA	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.3E+07
ERS3422234	B02320_T2	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	NA	3200	Mixed	Yes	No	NA	no	NA	no	No	Yes	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422235	B02320_T1	Infancy	Vaginal	Vaginal	6.80	3	B	Postnatal	Male	NA	3200	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422236	B02320_T2	Infancy	Vaginal	Vaginal	6.80	3	B	Postnatal	Male	NA	3200	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422237	B02322	Infancy	Vaginal	Vaginal	6.83	4	B	Postnatal	Female	35-40	4400	Mixed	Yes	No	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.2E+07	2E+07
ERS3422238	B02322	7	Vaginal	Vaginal	Neonatal	4	B	Postnatal	Female	35-40	4400	Mixed	Yes	No	NA	no	NA	no	Yes	No	normal_Bacteroides	2.2E+07	2E+07
ERS3422239	B02326	7	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Male	25-30	3400	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.8E+07
ERS3422240	B02326	21	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Male	25-30	3400	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3422241	B02326	4	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Male	25-30	3400	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.6E+07	2.2E+07
ERS3422242	B02326	Infancy	Caesarean	Emergency_	6.77	3	B	Postnatal	Male	25-30	3400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422243	B02329	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	25-30	3000	BF	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.8E+07	2.4E+07
ERS3422244	B02329	Infancy	Vaginal	Vaginal	6.73	2	B	Postnatal	Male	25-30	3000	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.5E+07
ERS3422245	B02358	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3500	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.6E+07	2.3E+07
ERS3422246	B02358	Mother	Vaginal	Vaginal	Mother	1	B	NA	Female	30-35	3500	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07

ERS3422247	B02358	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3500	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422248	B02358	Infancy	Vaginal	Vaginal	6.50	1	B	Postnatal	Female	30-35	3500	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422249	B02363	21	Caesarean	Emergency_	Neonatal	1	B	Postnatal	Male	30-35	3200	Mixed	Yes	Yes	Yes	no	NA	Yes	No	Yes	low_Bacteroides	2.3E+07	2E+07
ERS3422250	B02363	Infancy	Caesarean	Emergency_	6.57	1	B	Postnatal	Male	30-35	3200	Mixed	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.2E+07	1.9E+07
ERS3422251	B02369	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3100	NA	NA	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	2E+07
ERS3422256	B02369	Infancy	Vaginal	Vaginal	6.57	1	B	Postnatal	Female	30-35	3100	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.6E+07	1.3E+07
ERS3422257	B02382	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	3600	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.8E+07	2.5E+07
ERS3422258	B02382	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	3600	Mixed	Yes	No	NA	no	NA	no	No	Yes	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422259	B02382	Infancy	Vaginal	Vaginal	6.97	2	B	Postnatal	Female	35-40	3600	NA	NA	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422260	B02401	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	20-25	2800	BF	Yes	Yes	NA	no	Yes	no	No	No	low_Bacteroides	1.7E+07	1.4E+07
ERS3422261	B02401	Infancy	Vaginal	Vaginal	6.27	1	B	Postnatal	Male	20-25	2800	NA	NA	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422262	B02403	Infancy	Caesarean	Elective_CS	6.53	3	B	Postnatal	Female	30-35	4400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422263	B02403	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Female	30-35	4400	BF	Yes	No	Yes	no	NA	no	No	Yes	low_Bacteroides	1.9E+07	1.8E+07
ERS3422264	B02416	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	40-45	3300	BF	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422265	B02416	Infancy	Vaginal	Vaginal	6.17	0	B	Postnatal	Male	40-45	3300	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.6E+07
ERS3422266	B02429	Infancy	Vaginal	Vaginal	6.33	1	B	Postnatal	Male	25-30	3600	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422267	B02429	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	3600	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422268	B02447	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	2600	Mixed	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	1.5E+07	1.3E+07
ERS3422269	B02447	Infancy	Vaginal	Vaginal	5.70	1	B	Postnatal	Female	25-30	2600	NA	NA	No	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422270	B02448	7	Vaginal	Vaginal	Neonatal	0	B	Home	Male	25-30	3200	BF	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3422271	B02448	Infancy	Vaginal	Vaginal	9.20	0	B	Home	Male	25-30	3200	NA	NA	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.2E+07	2E+07
ERS3422272	B02450	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3200	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.8E+07	2.5E+07
ERS3422273	B02450	Infancy	Caesarean	Elective_CS	6.17	2	B	Postnatal	Female	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.8E+07
ERS3422274	B02457	21	Vaginal	Vaginal	Neonatal	0	B	Home	Male	25-30	4100	NoBF	No	No	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	2E+07
ERS3422275	B02457	Infancy	Vaginal	Vaginal	6.03	0	B	Home	Male	25-30	4100	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422276	B02458	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.6E+07
ERS3422277	B02458	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3100	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	1.3E+07	1E+07
ERS3422278	B02458	Mother	Caesarean	Elective_CS	Mother	2	B	NA	Female	35-40	3100	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3422279	B02486	Infancy	Vaginal	Vaginal	6.07	0	B	Home	Female	25-30	4400	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3422280	B02486	7	Vaginal	Vaginal	Neonatal	0	B	Home	Female	25-30	4400	Mixed	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3422281	B02493	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3800	BF	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.3E+07	2.2E+07
ERS3422282	B02493	Infancy	Vaginal	Vaginal	6.10	1	B	Postnatal	Female	30-35	3800	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.4E+07
ERS3422283	B02511	7	Caesarean	Elective_CS	Neonatal	4	B	Postnatal	Male	35-40	4100	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.7E+07
ERS3422284	B02511	Infancy	Caesarean	Elective_CS	5.97	4	B	Postnatal	Male	35-40	4100	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422285	B02528	Infancy	Vaginal	Vaginal	7.33	2	B	Postnatal	Female	35-40	2400	NA	NA	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422286	B02528	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	35-40	2400	NA	NA	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422287	B02540	4	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	25-30	2600	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	3E+07	2.5E+07
ERS3422288	B02540	21	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	25-30	2600	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	4.5E+07	3.6E+07
ERS3422289	B02540	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Female	25-30	2600	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.5E+07	2E+07
ERS3422290	B02542	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	25-30	3400	Mixed	Yes	No	NA	no	Yes	Yes	No	Yes	low_Bacteroides	2.9E+07	2.4E+07
ERS3422291	B02542	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	25-30	3400	Mixed	Yes	No	NA	no	Yes	Yes	No	Yes	low_Bacteroides	3.1E+07	2.6E+07
ERS3422292	B02542	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	25-30	3400	Mixed	Yes	No	NA	no	Yes	no	No	Yes	low_Bacteroides	2.7E+07	2.1E+07
ERS3422293	B02542	Infancy	Vaginal	Vaginal	5.67	2	B	Postnatal	Male	25-30	3400	Mixed	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422294	B02562	7	Caesarean	Elective_CS	Neonatal	3	B	Postnatal	Male	45-50	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3422295	B02562	Infancy	Caesarean	Elective_CS	7.30	3	B	Postnatal	Male	45-50	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422296	B02588	4	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	30-35	3600	BF	Yes	Yes	NA	no	NA	Yes	No	Yes	low_Bacteroides	3.7E+07	3.2E+07
ERS3422297	B02588	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	30-35	3600	BF	Yes	Yes	NA	no	NA	Yes	No	Yes	low_Bacteroides	3.7E+07	3E+07
ERS3422298	B02588	21	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	30-35	3600	Mixed	Yes	Yes	NA	no	NA	no	No	Yes	low_Bacteroides	1.2E+07	8000764
ERS3422299	B02607	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Male	40-45	3600	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422300	B02607	Infancy	Vaginal	Vaginal	7.23	0	B	Postnatal	Male	40-45	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422301	B02610	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	25-30	3000	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3422302	B02610	Infancy	Vaginal	Vaginal	7.17	2	B	Postnatal	Male	25-30	3000	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422303	B02613	7	Caesarean	Elective_CS	Neonatal	4	B	Postnatal	Female	25-30	2700	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.6E+07	1.5E+07
ERS3422304	B02613	Infancy	Caesarean	Elective_CS	7.00	4	B	Postnatal	Female	25-30	2700	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422305	B02618	Infancy	Caesarean	Elective_CS	7.13	4	B	Postnatal	Male	35-40	3600	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3422306	B02618	7	Caesarean	Elective_CS	Neonatal	4	B	Postnatal	Male	35-40	3600	Mixed	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.7E+07
ERS3422307	B02639_T2	7	Vaginal	Vaginal	Neonatal	5	B	Postnatal	Female	NA	2400	BF	Yes	No	NA	no	NA	Yes	No	Yes	normal_Bacteroides	2E+07	1.8E+07
ERS3422308	B02639_T1	7	Vaginal	Vaginal	Neonatal	5	B	Postnatal	Female	NA	2400	BF	Yes	No	NA	no	NA	Yes	No	Yes	low_Bacteroides	1.7E+07	1.4E+07
ERS3422309	B02639_T1	Infancy	Vaginal	Vaginal	7.20	5	B	Postnatal	Female	NA	2400	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422310	B02639_T2	Infancy	Vaginal	Vaginal	7.20	5	B	Postnatal	Female	NA	2400	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422311	B02657	Infancy	Vaginal	Vaginal	6.97	0	B	Postnatal	Female	40-45	3800	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422312	B02657	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Female	40-45	3800	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.8E+07
ERS3422313	B02669	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	40-45	3700	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.7E+07	1.4E+07
ERS3422314	B02669	Infancy	Caesarean	Elective_CS	7.00	2	B	Postnatal	Male	40-45	3700	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422315	B02685	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3800	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.7E+07	1.4E+07
ERS3422316	B02685	Infancy	Caesarean	Elective_CS	7.03	2	B	Postnatal	Female	35-40	3800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3422317	B02693	Infancy	Vaginal	Vaginal	7.17	2	B	Postnatal	Male	30-35	3100	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422318	B02693	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	30-35	3100	Mixed	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422319	B02697	Infancy	Vaginal	Vaginal	7.17	1	B	Postnatal	Male	25-30	3300	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422320	B02697	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	25-30	3300	Mixed	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.6E+07
ERS3422321	B02698	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	35-40	3100	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3422322	B02698	Infancy	Caesarean	Elective_CS	7.00	2	B	Postnatal	Female	35-40	3100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422323	B02708	7	Caesarean	Elective_CS	Neonatal	71	B	NICU	Male	30-35	1000	BF	Yes	No	Yes	no	NA	no	Yes	Yes	low_Bacteroides	1.9E+07	1.7E+07
ERS3422324	B02708	Infancy	Caesarean	Elective_CS	6.47	71	B	NICU	Male	30-35	1000	NA	NA	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3422325	B02712	Infancy	Caesarean	Emergency_	7.07	3	B	Postnatal	Male	30-35	3800	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422326	B02712	7	Caesarean	Emergency_	Neonatal	3	B	Postnatal	Male	30-35	3800	BF	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.3E+07	2.1E+07
ERS3422327	B02714	7	Vaginal	Vaginal	Neonatal	7	B	NICU	Male	30-35	2400	Mixed	Yes	No	NA	no	NA	no	Yes	No	low_Bacteroides	2.3E+07	2.1E+07
ERS3422328	B02714	Infancy	Vaginal	Vaginal	6.83	7	B	NICU	Male	30-35	2400	Mixed	Yes	No	NA	no	NA	no	Yes	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422329	B02720	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3900	BF	Yes	Yes	NA	no	Yes	no	No	No	low_Bacteroides	2.7E+07	2.1E+07
ERS3422330	B02720	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3900	BF	Yes	Yes	NA	no	Yes	no	No	No	low_Bacteroides	2.6E+07	2E+07
ERS3422331	B02720	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3900	BF	Yes	Yes	NA	no	Yes	no	No	No	low_Bacteroides	1.7E+07	1.3E+07
ERS3422332	B02722	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3800	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.4E+07	1.9E+07
ERS3422333	B02722	21	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3800	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	3.6E+07	2.9E+07
ERS3422334	B02722	4	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Female	30-35	3800	NoBF	No	No	Yes	no	NA	no	No	No	low_Bacteroides	4.8E+07	4.1E+07
ERS3422335	B02722	Infancy	Caesarean	Elective_CS	6.90	2	B	Postnatal	Female	30-35	3800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422336	B02724	21	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	2900	BF	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.8E+07	2.1E+07
ERS3422337	B02724	4	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	2900	Mixed	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	1.9E+07	1.5E+07
ERS3422338	B02724	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	2900	BF	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	1.9E+07	1.5E+07
ERS3422339	B02724	Infancy	Vaginal	Vaginal	7.73	1	B	Postnatal	Female	30-35	2900	Mixed	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.7E+07
ERS3422340	B02739	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	35-40	4700	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3422341	B02739	Infancy	Vaginal	Vaginal	7.00	3	B	Postnatal	Male	35-40	4700	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422342	B02741	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	3000	BF	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.7E+07
ERS3422343	B02741	Infancy	Vaginal	Vaginal	6.90	1	B	Postnatal	Female	25-30	3000	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422344	B02752	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Male	30-35	3600	Mixed	Yes	Yes	NA	no	NA	no	No	Yes	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422345	B02752	Infancy	Vaginal	Vaginal	6.87	2	B	Postnatal	Male	30-35	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.5E+07	2.2E+07
ERS3422346	B02765	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	25-30	2500	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2.3E+07	2.1E+07
ERS3422347	B02765	Infancy	Vaginal	Vaginal	6.87	1	B	Postnatal	Female	25-30	2500	Mixed	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.5E+07
ERS3422348	B02779	7	Caesarean	Elective_CS	Neonatal	2	B	Postnatal	Male	25-30	4100	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3422349	B02779	Infancy	Caesarean	Elective_CS	6.37	2	B	Postnatal	Male	25-30	4100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422350	B02780	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	30-35	3100	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2.3E+07	2.1E+07

ERS3422351	B02780	Infancy	Vaginal	Vaginal	6.87	2	B	Postnatal	Female	30-35	3100	Mixed	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.2E+07
ERS3422352	B02785	7	Vaginal	Vaginal	Neonatal	7	B	Postnatal	Male	35-40	3500	Mixed	Yes	No	NA	no	NA	Yes	Yes	Yes	normal_Bacteroides	2E+07	1.8E+07
ERS3422353	B02785	Infancy	Vaginal	Vaginal	6.70	7	B	Postnatal	Male	35-40	3500	Mixed	Yes	No	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422354	B02813	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Female	40-45	2400	BF	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3422355	B02813	Infancy	Vaginal	Vaginal	6.93	0	B	Postnatal	Female	40-45	2400	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422356	B02816	7	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Male	30-35	2800	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3422357	B02816	Infancy	Caesarean	Emergency_	6.87	2	B	Postnatal	Male	30-35	2800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422358	B02817	7	Caesarean	Emergency_	Neonatal	6	B	Postnatal	Female	35-40	3900	Mixed	Yes	No	Yes	no	NA	no	No	Yes	low_Bacteroides	2.2E+07	2E+07
ERS3422359	B02817	Infancy	Caesarean	Emergency_	6.57	6	B	Postnatal	Female	35-40	3900	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422360	B02821	7	Vaginal	Vaginal	Neonatal	7	B	Postnatal	Male	25-30	3700	NoBF	No	No	NA	no	NA	no	Yes	No	low_Bacteroides	1.6E+07	1.4E+07
ERS3422361	B02821	Infancy	Vaginal	Vaginal	6.73	7	B	Postnatal	Male	25-30	3700	NoBF	No	No	NA	no	NA	no	Yes	NA	low_Bacteroides	1.6E+07	1.4E+07
ERS3422362	B02832	Infancy	Vaginal	Vaginal	6.73	1	B	Postnatal	Male	30-35	2700	NoBF	No	No	NA	no	Yes	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422363	B02832	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	2700	NoBF	No	No	NA	no	Yes	no	No	No	low_Bacteroides	1.7E+07	1.5E+07
ERS3422364	B02834	7	Caesarean	Elective_CS	Neonatal	1	B	Postnatal	Male	30-35	3200	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.2E+07	2E+07
ERS3422365	B02834	Infancy	Caesarean	Elective_CS	6.53	1	B	Postnatal	Male	30-35	3200	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3422366	B02841	7	Caesarean	Emergency_	Neonatal	1	B	Postnatal	Male	30-35	4100	NoBF	No	No	Yes	no	NA	Yes	No	No	low_Bacteroides	1.3E+07	1.2E+07
ERS3422367	B02841	Infancy	Caesarean	Emergency_	6.80	1	B	Postnatal	Male	30-35	4100	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422368	B02842	7	Vaginal	Vaginal	Neonatal	0	B	Postnatal	Female	35-40	4400	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422369	B02842	Infancy	Vaginal	Vaginal	6.73	0	B	Postnatal	Female	35-40	4400	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422370	B02861	Infancy	Vaginal	Vaginal	6.47	1	B	Postnatal	Female	30-35	3800	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422371	B02861	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Female	30-35	3800	NA	NA	No	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.8E+07
ERS3422372	B02885	7	Vaginal	Vaginal	Neonatal	0	B	Home	Male	40-45	3200	BF	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	1.7E+07	1.5E+07
ERS3422373	B02885	Infancy	Vaginal	Vaginal	6.43	0	B	Home	Male	40-45	3200	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422374	B02909	7	Caesarean	Emergency_	Neonatal	2	B	Postnatal	Female	30-35	4100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422375	B02909	Infancy	Caesarean	Emergency_	6.53	2	B	Postnatal	Female	30-35	4100	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.4E+07
ERS3422376	B02932	7	Vaginal	Vaginal	Neonatal	3	B	Postnatal	Male	35-40	2900	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422377	B02932	Infancy	Vaginal	Vaginal	6.40	3	B	Postnatal	Male	35-40	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422378	B02935	7	Vaginal	Vaginal	Neonatal	2	B	Postnatal	Female	25-30	2900	NA	NA	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.3E+07
ERS3422379	B02935	Infancy	Vaginal	Vaginal	6.40	2	B	Postnatal	Female	25-30	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	2.1E+07
ERS3422380	B02939	7	Vaginal	Vaginal	Neonatal	1	B	Postnatal	Male	30-35	3700	Mixed	Yes	No	NA	no	NA	no	No	Yes	low_Bacteroides	1.8E+07	1.6E+07
ERS3422381	B02939	Infancy	Vaginal	Vaginal	6.40	1	B	Postnatal	Male	30-35	3700	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.4E+07
ERS3422382	S1	4	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	Yes	NA	no	NA	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422383	S1	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	Yes	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3422384	S10	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.8E+07	2.6E+07
ERS3422385	S10	Mother	Caesarean	Elective_CS	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3422386	S11	4	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422387	S12	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	1.6E+07	1.5E+07
ERS3422388	S13	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	Yes	NA	no	NA	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422389	S13	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	Yes	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3422390	S16	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.2E+07	2E+07
ERS3422391	S17	7	Caesarean	Emergency_	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.9E+07	2.7E+07
ERS3422392	S19	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3422393	S2	7	Caesarean	Emergency_	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	Yes	Yes	NA	no	NA	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422394	S20	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.7E+07	2.5E+07
ERS3422395	S21	4	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	3.3E+07	3E+07
ERS3422396	S23	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	1.5E+07	1.4E+07
ERS3422397	S3	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	3E+07	2.8E+07
ERS3422398	S3	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.1E+07	1.8E+07
ERS3422399	S33	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422400	S33	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3422401	S34	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422402	S34	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3422403	S37_T1	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3422404	S37_T2	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422405	S39	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3422406	S4	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.7E+07	2.5E+07
ERS3422407	S41	4	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422408	S44	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	NoBF	No	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422409	S45	7	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422410	S6	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	BF	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.6E+07	2.4E+07
ERS3422411	S7	7	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	low_Bacteroides	2.9E+07	2.6E+07
ERS3422412	S7	Mother	Vaginal	Vaginal	Mother	NA	A	NA	NA	NA	NA	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.1E+07	1.9E+07
ERS3422413	S8	21	Vaginal	Vaginal	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	NA	no	NA	no	NA	NA	normal_Bacteroides	2.8E+07	2.5E+07
ERS3422414	S9	4	Caesarean	Elective_CS	Neonatal	NA	A	NA	NA	NA	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3422415	C01007	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	30-35	3000	NA	NA	NA	No	no	No	no	NA	NA	NA	2.1E+07	1.8E+07
ERS3422416	C01007	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	30-35	3000	BF	Yes	No	No	no	No	no	No	NA	normal_Bacteroides	2.4E+07	1.9E+07
ERS3422417	C01007	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	30-35	3000	BF	Yes	No	No	no	No	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422418	C01008_T1	21	Vaginal	Vaginal	Neonatal	0	C	Postnatal	Male	NA	2900	Mixed	Yes	No	No	no	No	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3422419	C01008_T2	21	Vaginal	Vaginal	Neonatal	0	C	Postnatal	Male	NA	2900	Mixed	Yes	No	No	no	No	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422420	C01008_T2	7	Vaginal	Vaginal	Neonatal	0	C	Postnatal	Male	NA	2900	Mixed	Yes	No	No	no	No	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422421	C01008_T1	4	Vaginal	Vaginal	Neonatal	0	C	Postnatal	Male	NA	2900	Mixed	Yes	No	No	no	No	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422422	C01008_T2	4	Vaginal	Vaginal	Neonatal	0	C	Postnatal	Male	NA	2900	Mixed	Yes	No	No	no	No	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422423	C01008_T1	7	Vaginal	Vaginal	Neonatal	0	C	Postnatal	Male	NA	2900	Mixed	Yes	No	No	no	No	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422424	C01010	Mother	Caesarean	Elective_CS	Mother	1	C	NA	Female	30-35	4300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.6E+07	2.2E+07
ERS3422425	C01010	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	30-35	4300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3E+07	2.6E+07
ERS3422426	C01012	7	Caesarean	Emergency_	Neonatal	5	C	Postnatal	Male	30-35	3500	BF	Yes	No	Yes	no	NA	no	Yes	No	low_Bacteroides	2.2E+07	1.9E+07
ERS3422427	C01012	21	Caesarean	Emergency_	Neonatal	5	C	Postnatal	Male	30-35	3500	BF	Yes	No	Yes	no	NA	no	Yes	No	low_Bacteroides	2.4E+07	1.9E+07
ERS3422428	C01012	Mother	Caesarean	Emergency_	Mother	5	C	NA	Male	30-35	3500	NA	NA	NA	Yes	no	NA	no	Yes	NA	NA	2.3E+07	2E+07
ERS3422429	C01052	Mother	Vaginal	Vaginal	Mother	3	C	NA	Female	35-40	3300	NA	NA	NA	No	no	Yes	no	NA	NA	NA	2.5E+07	2.1E+07
ERS3422430	C01052	7	Vaginal	Vaginal	Neonatal	3	C	Postnatal	Female	35-40	3300	Mixed	Yes	No	No	no	Yes	no	No	NA	normal_Bacteroides	2.6E+07	2.2E+07
ERS3422431	C01052	4	Vaginal	Vaginal	Neonatal	3	C	Postnatal	Female	35-40	3300	Mixed	Yes	No	No	no	Yes	no	No	NA	normal_Bacteroides	2.1E+07	1.7E+07
ERS3422432	C01052	21	Vaginal	Vaginal	Neonatal	3	C	Postnatal	Female	35-40	3300	Mixed	Yes	No	No	no	Yes	no	No	NA	normal_Bacteroides	2.7E+07	2.3E+07
ERS3422433	C01070	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	35-40	3200	Mixed	Yes	No	No	no	Yes	no	No	NA	normal_Bacteroides	2.6E+07	2.3E+07
ERS3422434	C01070	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	35-40	3200	Mixed	Yes	No	No	no	Yes	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422435	C01070	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	35-40	3200	Mixed	Yes	No	No	no	Yes	no	No	NA	normal_Bacteroides	1.8E+07	1.5E+07
ERS3422436	C01075	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	20-25	3000	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.5E+07	2.1E+07
ERS3422437	C01075	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	20-25	3000	BF	Yes	Yes	NA	no	Yes	no	No	No	normal_Bacteroides	2.4E+07	2E+07
ERS3422438	C01075	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	20-25	3000	Mixed	Yes	Yes	NA	no	Yes	no	No	No	normal_Bacteroides	2.5E+07	2.1E+07
ERS3422439	C01138	Mother	Caesarean	Emergency_	Mother	2	C	NA	Male	40-45	3300	NA	NA	NA	Yes	no	NA	no	Yes	NA	NA	2.1E+07	1.8E+07
ERS3422440	C01138	4	Caesarean	Emergency_	Neonatal	2	C	Postnatal	Male	40-45	3300	Mixed	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422441	C01138	7	Caesarean	Emergency_	Neonatal	2	C	Postnatal	Male	40-45	3300	Mixed	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422442	C01201	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	25-30	2900	NA	NA	NA	No	no	No	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3422443	C01201	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	25-30	2900	Mixed	Yes	Yes	No	no	No	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422444	C01201	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	25-30	2900	Mixed	Yes	Yes	No	no	No	no	No	NA	normal_Bacteroides	2.4E+07	2.1E+07
ERS3422445	C01202	7	Caesarean	Emergency_	Neonatal	1	C	Postnatal	Female	40-45	3400	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422446	C01202	Infancy	Caesarean	Emergency_	12.50	1	C	Postnatal	Female	40-45	3400	NA	NA	No	Yes	no	No	no	No	No	low_Bacteroides	2E+07	1.8E+07
ERS3422447	C01204	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3000	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.2E+07
ERS3422448	C01204	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3000	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422449	C01204	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	30-35	3000	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3422450	C01204	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3000	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07

ERS3422451	C01204	Infancy	Vaginal	Vaginal	14.17	1	C	Postnatal	Male	30-35	3000	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422452	C01288	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	35-40	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422453	C01288	Infancy	Vaginal	Vaginal	11.90	1	C	Postnatal	Male	35-40	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.9E+07
ERS3422454	C01329	Mother	Caesarean	Elective_CS	Mother	1	C	NA	Male	40-45	3400	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	1.7E+07	1.6E+07
ERS3422455	C01329	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	40-45	3400	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.5E+07
ERS3422456	C01329	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	40-45	3400	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.5E+07	1.4E+07
ERS3422457	C01329	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	40-45	3400	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3422458	C01331	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	30-35	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.5E+07
ERS3422459	C01331	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	30-35	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.5E+07
ERS3422460	C01331	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	30-35	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.6E+07
ERS3422461	C01352	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	30-35	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422462	C01352	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	30-35	3100	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422463	C01381	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	25-30	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422464	C01381	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	25-30	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422465	C01381	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	25-30	3500	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.6E+07	2.2E+07
ERS3422466	C01381	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	25-30	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.4E+07	1.3E+07
ERS3422467	C01382	21	Caesarean	Emergency	Neonatal	37	C	NNU	Female	35-40	1800	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422468	C01382	7	Caesarean	Emergency	Neonatal	37	C	NNU	Female	35-40	1800	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422469	C01382	Infancy	Caesarean	Emergency_	11.93	37	C	NNU	Female	35-40	1800	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3422470	C01384	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	30-35	3000	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.4E+07	1.2E+07
ERS3422471	C01384	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	30-35	3000	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.7E+07	1.6E+07
ERS3422472	C01384	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	30-35	3000	BF	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.4E+07	1.4E+07
ERS3422473	C01386	7	Caesarean	Elective_CS	Neonatal	2	C	Postnatal	Female	35-40	3400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422474	C01386	21	Caesarean	Elective_CS	Neonatal	2	C	Postnatal	Female	35-40	3400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422475	C01387	21	Vaginal	Vaginal	Neonatal	20	C	NNU	Male	35-40	2400	BF	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3422476	C01387	4	Vaginal	Vaginal	Neonatal	20	C	NNU	Male	35-40	2400	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	1.3E+07	1.2E+07
ERS3422477	C01387	Mother	Vaginal	Vaginal	Mother	20	C	NA	Male	35-40	2400	NA	NA	NA	NA	no	Yes	no	Yes	NA	NA	1.5E+07	1.4E+07
ERS3422478	C01387	7	Vaginal	Vaginal	Neonatal	20	C	NNU	Male	35-40	2400	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	1.6E+07	1.3E+07
ERS3422479	C01387	Infancy	Vaginal	Vaginal	13.20	20	C	NNU	Male	35-40	2400	Mixed	Yes	No	NA	no	Yes	no	Yes	No	low_Bacteroides	1.7E+07	1.6E+07
ERS3422480	C01389	Mother	Caesarean	Elective_CS	Mother	1	C	NA	Female	35-40	2300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	1.9E+07	1.8E+07
ERS3422481	C01389	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	35-40	2300	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3422482	C01389	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	35-40	2300	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.4E+07
ERS3422483	C01389	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	35-40	2300	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.2E+07	1.2E+07
ERS3422495	C01390	Mother	Caesarean	Elective_CS	Mother	2	C	NA	Male	30-35	3000	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	1.7E+07	1.6E+07
ERS3422496	C01390	7	Caesarean	Elective_CS	Neonatal	2	C	MCU	Male	30-35	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422497	C01390	4	Caesarean	Elective_CS	Neonatal	2	C	MCU	Male	30-35	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3422498	C01392	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	40-45	3600	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.6E+07	3E+07
ERS3422499	C01392	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	40-45	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.4E+07
ERS3422500	C01392	Infancy	Caesarean	Elective_CS	11.87	1	C	Postnatal	Female	40-45	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.7E+07
ERS3422501	C01429	4	Caesarean	Emergency	Neonatal	5	C	NNU	Male	35-40	3400	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422502	C01429	Infancy	Caesarean	Emergency_	11.47	5	C	NNU	Male	35-40	3400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.6E+07
ERS3422503	C01442	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3500	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422484	C01442	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3500	BF	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	1.7E+07	1.6E+07
ERS3422485	C01442	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3500	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	1.6E+07	1.5E+07
ERS3422486	C01442	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	30-35	3500	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.3E+07	2E+07
ERS3422487	C01443	Mother	Caesarean	Emergency	Mother	5	C	NA	Male	35-40	3500	NA	NA	NA	Yes	no	No	no	NA	NA	NA	1.6E+07	1.5E+07
ERS3422488	C01443	7	Caesarean	Emergency	Neonatal	5	C	MCU	Male	35-40	3500	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.5E+07	1.4E+07
ERS3422489	C01443	Infancy	Caesarean	Emergency_	11.00	5	C	MCU	Male	35-40	3500	NA	NA	No	Yes	no	No	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3422490	C01444	21	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	35-40	4100	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.4E+07	1.3E+07
ERS3422491	C01444	4	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	35-40	4100	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3422492	C01444	7	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	35-40	4100	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422493	C01447_T2	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	NA	2700	Mixed	Yes	Yes	NA	no	NA	no	Yes	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422494	C01447_T2	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	NA	2700	Mixed	Yes	Yes	NA	no	NA	no	Yes	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422504	C01447_T2	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	NA	2700	Mixed	Yes	Yes	NA	no	NA	no	Yes	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422505	C01447_T1	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	NA	2700	Mixed	Yes	Yes	NA	no	NA	no	Yes	NA	low_Bacteroides	3.1E+07	2.5E+07
ERS3422506	C01447_T1	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	NA	2700	Mixed	Yes	Yes	NA	no	NA	no	Yes	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3422507	C01478	21	Vaginal	Vaginal	Neonatal	10	C	NNU	Male	35-40	1700	BF	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422508	C01478	Infancy	Vaginal	Vaginal	11.20	10	C	NNU	Male	35-40	1700	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422509	C01485	7	Vaginal	Vaginal	Neonatal	6	C	NNU	Male	40-45	3200	Mixed	Yes	No	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422510	C01485	21	Vaginal	Vaginal	Neonatal	6	C	NNU	Male	40-45	3200	Mixed	Yes	No	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.2E+07	2E+07
ERS3422511	C01485	Mother	Vaginal	Vaginal	Mother	6	C	NA	Male	40-45	3200	NA	NA	NA	NA	no	NA	no	Yes	NA	NA	2.2E+07	1.9E+07
ERS3422512	C01488	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	35-40	2700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.5E+07
ERS3422513	C01488	Mother	Caesarean	Elective_CS	Mother	1	C	NA	Female	35-40	2700	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	1.6E+07	1.5E+07
ERS3422514	C01512	4	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Male	35-40	3800	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3422515	C01512	Infancy	Vaginal	Vaginal	11.27	2	C	Postnatal	Male	35-40	3800	NA	NA	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3422516	C01528	21	Caesarean	Elective_CS	Neonatal	2	C	NA	Male	35-40	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422517	C01528	4	Caesarean	Elective_CS	Neonatal	2	C	NA	Male	35-40	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.3E+07
ERS3422518	C01528	7	Caesarean	Elective_CS	Neonatal	2	C	NA	Male	35-40	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422519	C01529	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	40-45	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422520	C01529	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	40-45	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3422521	C01529	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	40-45	3300	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422522	C01530	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	30-35	3500	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.6E+07
ERS3422523	C01530	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	30-35	3500	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422524	C01530	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	30-35	3500	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422525	C01530	Infancy	Caesarean	Elective_CS	10.80	1	C	Postnatal	Female	30-35	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	1.6E+07	1.5E+07
ERS3422526	C01531	7	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Female	35-40	4300	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422527	C01531	4	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Female	35-40	4300	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422528	C01531	Infancy	Vaginal	Vaginal	10.53	2	C	Postnatal	Female	35-40	4300	NoBF	No	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.2E+07
ERS3422529	C01560	7	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Female	40-45	2700	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422530	C01560	Mother	Vaginal	Vaginal	Mother	2	C	NA	Female	40-45	2700	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3422531	C01654	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3500	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.2E+07
ERS3422532	C01654	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3500	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.4E+07	2E+07
ERS3422533	C01654	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3500	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.6E+07
ERS3422534	C01658	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	25-30	2900	BF	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3422535	C01658	Infancy	Vaginal	Vaginal	10.20	1	C	Postnatal	Male	25-30	2900	Mixed	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422536	C01660	7	Caesarean	Emergency_	Neonatal	2	C	Postnatal	Male	25-30	2600	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3422537	C01660	Infancy	Caesarean	Emergency_	10.53	2	C	Postnatal	Male	25-30	2600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422538	C01661	21	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	40-45	3000	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422539	C01661	Infancy	Caesarean	Elective_CS	10.23	1	C	MCU	Male	40-45	3000	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.2E+07	1.8E+07
ERS3422540	C01662	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3422541	C01662	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422542	C01667	7	Caesarean	Elective_CS	Neonatal	2	C	Postnatal	Male	NA	3400	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422543	C01667	4	Caesarean	Elective_CS	Neonatal	2	C	Postnatal	Male	NA	3400	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422544	C01667	21	Caesarean	Elective_CS	Neonatal	2	C	Postnatal	Male	NA	3400	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422545	C01689	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	40-45	2900	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2E+07
ERS3422546	C01689	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	40-45	2900	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.1E+07
ERS3422547	C01689	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	40-45	2900	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.4E+07
ERS3422548	C01690	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	35-40	3200	BF	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422549	C01690	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	35-40	3200	BF	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422550	C01690	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	35-40	3200	BF	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.4E+07	2E+07

ERS3422551	C01690	Infancy	Vaginal	Vaginal	9.93	1	C	Postnatal	Male	35-40	3200	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422552	C01695	21	Caesarean	Elective_CS	Neonatal	3	C	MCU	Female	35-40	3600	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3422553	C01695	4	Caesarean	Elective_CS	Neonatal	3	C	MCU	Female	35-40	3600	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.3E+07
ERS3422554	C01695	7	Caesarean	Elective_CS	Neonatal	3	C	MCU	Female	35-40	3600	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422555	C01695	Infancy	Caesarean	Elective_CS	10.20	3	C	MCU	Female	35-40	3600	NA	NA	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422556	C01696	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	40-45	3600	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422557	C01696	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	40-45	3600	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422558	C01696	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	40-45	3600	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.1E+07	1.8E+07
ERS3422559	C01696	Infancy	Vaginal	Vaginal	9.93	1	C	Postnatal	Male	40-45	3600	NA	NA	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3422560	C01697	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	25-30	3200	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	3E+07	2.8E+07
ERS3422561	C01697	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	25-30	3200	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422562	C01697	Infancy	Vaginal	Vaginal	9.93	1	C	Postnatal	Male	25-30	3200	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422563	C01700	21	Caesarean	Emergency_	Neonatal	1	C	MCU	Female	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422564	C01700	4	Caesarean	Emergency_	Neonatal	1	C	MCU	Female	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.4E+07
ERS3422565	C01700	7	Caesarean	Emergency_	Neonatal	1	C	MCU	Female	35-40	3100	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422566	C01748_T1	4	Caesarean	Elective_CS	Neonatal	3	C	MCU	Male	NA	3000	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2.1E+07
ERS3422567	C01748_T2	4	Caesarean	Elective_CS	Neonatal	3	C	MCU	Male	NA	3000	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	2E+07
ERS3422568	C01748_T2	21	Caesarean	Elective_CS	Neonatal	3	C	MCU	Male	NA	3000	NoBF	No	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3422569	C01748_T1	Infancy	Caesarean	Elective_CS	9.80	3	C	MCU	Male	NA	3000	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.4E+07
ERS3422570	C01748_T2	Infancy	Caesarean	Elective_CS	9.80	3	C	MCU	Male	NA	3000	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3422571	C01749	7	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Female	40-45	3600	BF	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.4E+07	2.1E+07
ERS3422572	C01749	21	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Female	40-45	3600	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422573	C01749	Infancy	Vaginal	Vaginal	10.07	2	C	Postnatal	Female	40-45	3600	Mixed	Yes	Yes	NA	no	Yes	no	No	No	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422574	C01750	7	Vaginal	Vaginal	Neonatal	1	C	BBC	Female	35-40	2700	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422575	C01750	Infancy	Vaginal	Vaginal	10.10	1	C	BBC	Female	35-40	2700	NA	NA	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422576	C01751	21	Caesarean	Emergency_	Neonatal	2	C	COB	Male	30-35	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422577	C01751	4	Caesarean	Emergency_	Neonatal	2	C	COB	Male	30-35	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422578	C01751	7	Caesarean	Emergency_	Neonatal	2	C	COB	Male	30-35	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422579	C01751	Infancy	Caesarean	Emergency_	10.43	2	C	COB	Male	30-35	4000	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422580	C01752	4	Vaginal	Vaginal	Neonatal	1	C	MCU	Female	35-40	3700	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422581	C01752	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	35-40	3700	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3422582	C01752	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Female	35-40	3700	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3422583	C01753	4	Vaginal	Vaginal	Neonatal	2	C	MCU	Female	30-35	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422584	C01753	7	Vaginal	Vaginal	Neonatal	2	C	MCU	Female	30-35	3500	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	2E+07
ERS3422585	C01753	Infancy	Vaginal	Vaginal	9.87	2	C	MCU	Female	30-35	3500	NA	NA	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422586	C01756	7	Caesarean	Emergency_	Neonatal	NA	C	NA	Female	40-45	3000	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	3.2E+07	2.7E+07
ERS3422587	C01756	Mother	Caesarean	Emergency_	Mother	NA	C	NA	Female	40-45	3000	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	3.2E+07	2.7E+07
ERS3422588	C01756	4	Caesarean	Emergency_	Neonatal	NA	C	NA	Female	40-45	3000	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	3.4E+07	2.9E+07
ERS3422589	C01756	21	Caesarean	Emergency_	Neonatal	NA	C	NA	Female	40-45	3000	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	3.2E+07	2.5E+07
ERS3422590	C01756	Infancy	Caesarean	Emergency_	9.60	NA	C	NA	Female	40-45	3000	Mixed	Yes	NA	Yes	no	NA	no	NA	No	low_Bacteroides	1.6E+07	1.5E+07
ERS3422591	C01757	4	Caesarean	Emergency_	Neonatal	1	C	MCU	Male	35-40	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422592	C01757	Mother	Caesarean	Emergency_	Mother	1	C	NA	Male	35-40	3600	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3422593	C01757	21	Caesarean	Emergency_	Neonatal	1	C	MCU	Male	35-40	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.4E+07
ERS3422594	C01757	Infancy	Caesarean	Emergency_	9.60	1	C	MCU	Male	35-40	3600	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3422595	C01758	21	Vaginal	Vaginal	Neonatal	1	C	MCU	Female	35-40	3800	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422596	C01758	4	Vaginal	Vaginal	Neonatal	1	C	MCU	Female	35-40	3800	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3422597	C01758	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Female	35-40	3800	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3422598	C01758	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	35-40	3800	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.3E+07	2E+07
ERS3422599	C01758	Infancy	Vaginal	Vaginal	10.20	1	C	MCU	Female	35-40	3800	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3422600	C01831	4	Caesarean	Emergency_	Neonatal	3	C	MCU	Male	35-40	2400	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3422601	C01831	Mother	Caesarean	Emergency_	Mother	3	C	NA	Male	35-40	2400	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.1E+07	1.8E+07
ERS3422602	C01831	21	Caesarean	Emergency_	Neonatal	3	C	MCU	Male	35-40	2400	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	3.2E+07	2.7E+07
ERS3422603	C01831	Infancy	Caesarean	Emergency_	NA	3	C	MCU	Male	35-40	2400	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.5E+07
ERS3422604	C01832	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	35-40	3900	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3422605	C01832	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	35-40	3900	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422606	C01832	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	35-40	3900	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422607	C01832	Infancy	Vaginal	Vaginal	10.03	1	C	Postnatal	Male	35-40	3900	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422608	C01834	21	Caesarean	Emergency_	Neonatal	1	C	Postnatal	Male	40-45	4100	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422609	C01834	Infancy	Caesarean	Emergency_	9.57	1	C	Postnatal	Male	40-45	4100	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3422610	C01836	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	25-30	3100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3422611	C01836	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	25-30	3100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.6E+07
ERS3422612	C01836	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Female	25-30	3100	BF	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3422613	C01837	21	Caesarean	Emergency_	Neonatal	3	C	Postnatal	Male	40-45	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	normal_Bacteroides	3.5E+07	3E+07
ERS3422614	C01837	4	Caesarean	Emergency_	Neonatal	3	C	Postnatal	Male	40-45	3500	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	normal_Bacteroides	3.3E+07	2.8E+07
ERS3422615	C01839	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	35-40	3800	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422616	C01839	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	35-40	3800	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422617	C01839	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	35-40	3800	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422618	C01839	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	35-40	3800	NA	NA	NA	NA	no	NA	no	NA	NA	NA	3.1E+07	2.6E+07
ERS3422619	C01840	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	30-35	3200	Mixed	Yes	NA	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422620	C01840	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	30-35	3200	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2E+07
ERS3422621	C01840	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	30-35	3200	Mixed	Yes	NA	NA	no	NA	no	No	NA	normal_Bacteroides	2.8E+07	2.3E+07
ERS3422622	C01840	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	30-35	3200	Mixed	Yes	NA	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.2E+07
ERS3422623	C01840	Infancy	Vaginal	Vaginal	9.47	1	C	Postnatal	Female	30-35	3200	Mixed	Yes	NA	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422624	C01841	21	Vaginal	Vaginal	Neonatal	3	C	TC	Female	40-45	2000	Mixed	Yes	Yes	NA	Yes	Yes	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3422625	C01841	4	Vaginal	Vaginal	Neonatal	3	C	TC	Female	40-45	2000	Mixed	Yes	Yes	NA	Yes	Yes	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3422626	C01841	7	Vaginal	Vaginal	Neonatal	3	C	TC	Female	40-45	2000	Mixed	Yes	Yes	NA	Yes	Yes	no	No	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3422627	C01841	Mother	Vaginal	Vaginal	Mother	3	C	NA	Female	40-45	2000	NA	NA	NA	NA	Yes	Yes	no	NA	NA	NA	2.4E+07	2E+07
ERS3422628	C01841	Infancy	Vaginal	Vaginal	9.90	3	C	TC	Female	40-45	2000	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422629	C01843	Infancy	Vaginal	Vaginal	9.93	2	C	Postnatal	Male	30-35	3200	NA	NA	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.3E+07	2.2E+07
ERS3422630	C01843	7	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Male	30-35	3200	BF	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422631	C01844	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	40-45	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.5E+07
ERS3422632	C01844	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	40-45	3600	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.9E+07	2.3E+07
ERS3422633	C01844	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	40-45	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.7E+07
ERS3422634	C01844	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	40-45	3600	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.6E+07	2.1E+07
ERS3422635	C01844	Infancy	Vaginal	Vaginal	9.43	1	C	Postnatal	Male	40-45	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.4E+07
ERS3422636	C01846	21	Vaginal	Vaginal	Neonatal	1	C	MCU	Female	30-35	3200	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2.6E+07	2.1E+07
ERS3422637	C01846	4	Vaginal	Vaginal	Neonatal	1	C	MCU	Female	30-35	3200	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	1.2E+07	8777514
ERS3422638	C01871	21	Vaginal	Vaginal	Neonatal	3	C	MCU	Female	25-30	3100	BF	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.1E+07	1.7E+07
ERS3422639	C01871	4	Vaginal	Vaginal	Neonatal	3	C	MCU	Female	25-30	3100	BF	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422640	C01871	7	Vaginal	Vaginal	Neonatal	3	C	MCU	Female	25-30	3100	BF	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.1E+07	1.7E+07
ERS3422641	C01871	Mother	Vaginal	Vaginal	Mother	3	C	NA	Female	25-30	3100	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	1.8E+07	1.5E+07
ERS3422642	C01873	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Male	40-45	2900	Mixed	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422643	C01873	21	Vaginal	Vaginal	Neonatal	1	C	MCU	Male	40-45	2900	Mixed	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422644	C01873	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	40-45	2900	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.1E+07	1.9E+07
ERS3422645	C01873	Infancy	Vaginal	Vaginal	9.27	1	C	MCU	Male	40-45	2900	Mixed	Yes	No	NA	no	Yes	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3422646	C01877	21	Caesarean	Elective_CS	Neonatal	1	C	MCU	Female	35-40	2700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3422647	C01877	4	Caesarean	Elective_CS	Neonatal	1	C	MCU	Female	35-40	2700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3E+07	2.6E+07
ERS3422648	C01877	7	Caesarean	Elective_CS	Neonatal	1	C	MCU	Female	35-40	2700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3422649	C01913	21	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	30-35	3500	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422650	C01913	4	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	30-35	3500	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.3E+07

ERS3422651	C01913	7	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	30-35	3500	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3422652	C01913	Infancy	Caesarean	Elective_CS	9.53	1	C	MCU	Male	30-35	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422653	C01914	7	Caesarean	Emergency_	Neonatal	3	C	MCU	Male	30-35	3900	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3422654	C01914	Mother	Caesarean	Emergency_	Mother	3	C	NA	Male	30-35	3900	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.1E+07	1.7E+07
ERS3422655	C01914	4	Caesarean	Emergency_	Neonatal	3	C	MCU	Male	30-35	3900	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3422656	C01915	21	Vaginal	Vaginal	Neonatal	3	C	MCU	Male	30-35	3100	Mixed	Yes	Yes	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422657	C01915	4	Vaginal	Vaginal	Neonatal	3	C	MCU	Male	30-35	3100	Mixed	Yes	Yes	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422658	C01915	7	Vaginal	Vaginal	Neonatal	3	C	MCU	Male	30-35	3100	Mixed	Yes	Yes	NA	no	NA	no	Yes	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422659	C01915	Infancy	Vaginal	Vaginal	11.57	3	C	MCU	Male	30-35	3100	Mixed	Yes	Yes	NA	no	NA	no	Yes	NA	normal_Bacteroides	1.8E+07	1.6E+07
ERS3422660	C01916	7	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Male	40-45	4300	NA	NA	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.9E+07	2.4E+07
ERS3422661	C01916	Mother	Vaginal	Vaginal	Mother	2	C	NA	Male	40-45	4300	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.6E+07	2.2E+07
ERS3422662	C01916	21	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Male	40-45	4300	NA	NA	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422663	C01917	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	40-45	3500	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.1E+07	8708008
ERS3422664	C01917	4	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	40-45	3500	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422665	C01917	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	40-45	3500	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422666	C01917	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	40-45	3500	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.1E+07	1.8E+07
ERS3422667	C01917	Infancy	Vaginal	Vaginal	10.20	1	C	Postnatal	Female	40-45	3500	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.9E+07	1.7E+07
ERS3422668	C01919	4	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	35-40	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3E+07	2.6E+07
ERS3422669	C01919	7	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	35-40	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.9E+07	2.5E+07
ERS3422670	C01919	Mother	Caesarean	Elective_CS	Mother	1	C	NA	Male	35-40	3600	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.6E+07	2.2E+07
ERS3422671	C01919	21	Caesarean	Elective_CS	Neonatal	1	C	Postnatal	Male	35-40	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422672	C01919	Infancy	Caesarean	Elective_CS	9.13	1	C	Postnatal	Male	35-40	3600	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.8E+07
ERS3422673	C01929	21	Vaginal	Vaginal	Neonatal	2	C	MCU	Female	30-35	3900	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3422674	C01929	4	Vaginal	Vaginal	Neonatal	2	C	MCU	Female	30-35	3900	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.8E+07
ERS3422675	C01929	7	Vaginal	Vaginal	Neonatal	2	C	MCU	Female	30-35	3900	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422676	C01929	Mother	Vaginal	Vaginal	Mother	2	C	NA	Female	30-35	3900	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3422677	C01930	21	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3422678	C01930	4	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.8E+07	2.4E+07
ERS3422679	C01930	7	Caesarean	Elective_CS	Neonatal	1	C	MCU	Male	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.1E+07
ERS3422680	C01930	Mother	Caesarean	Elective_CS	Mother	1	C	NA	Male	30-35	3200	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.3E+07	1.9E+07
ERS3422681	C01930	Infancy	Caesarean	Elective_CS	8.90	1	C	MCU	Male	30-35	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2E+07	1.7E+07
ERS3422682	C01931	21	Caesarean	Emergency_	Neonatal	4	C	MCU	Female	40-45	3700	BF	Yes	Yes	Yes	no	NA	no	Yes	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422683	C01931	Infancy	Caesarean	Emergency_	9.50	4	C	MCU	Female	40-45	3700	NA	NA	Yes	Yes	no	NA	no	Yes	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422684	C01959	21	Caesarean	Elective_CS	Neonatal	5	C	MCU	Male	30-35	3700	BF	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422685	C01959	Mother	Caesarean	Elective_CS	Mother	5	C	NA	Male	30-35	3700	NA	NA	NA	Yes	no	NA	no	Yes	NA	NA	2.2E+07	1.9E+07
ERS3422686	C01959	Infancy	Caesarean	Elective_CS	8.73	5	C	MCU	Male	30-35	3700	Mixed	Yes	No	Yes	no	NA	no	Yes	NA	low_Bacteroides	2.2E+07	1.9E+07
ERS3422687	C01960	7	Caesarean	Emergency_	Neonatal	1	C	Postnatal	Male	35-40	3400	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.8E+07	3.5E+07
ERS3422688	C01960	Infancy	Caesarean	Emergency_	8.73	1	C	Postnatal	Male	35-40	3400	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	1.9E+07
ERS3422689	C01960	Mother	Caesarean	Emergency_	Mother	1	C	NA	Male	35-40	3400	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3422690	C01962	21	Vaginal	Vaginal	Neonatal	2	C	MCU	Male	30-35	4100	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422691	C01962	4	Vaginal	Vaginal	Neonatal	2	C	MCU	Male	30-35	4100	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422692	C01962	7	Vaginal	Vaginal	Neonatal	2	C	MCU	Male	30-35	4100	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422693	C01962	Mother	Vaginal	Vaginal	Mother	2	C	NA	Male	30-35	4100	NA	NA	NA	NA	no	Yes	no	Yes	NA	NA	2.3E+07	1.9E+07
ERS3422694	C01962	Infancy	Vaginal	Vaginal	8.73	2	C	MCU	Male	30-35	4100	NA	NA	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422695	C01990	21	Vaginal	Vaginal	Neonatal	2	C	NNU	Female	35-40	3200	BF	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2E+07	1.6E+07
ERS3422696	C01990	4	Vaginal	Vaginal	Neonatal	2	C	NNU	Female	35-40	3200	BF	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422697	C01990	7	Vaginal	Vaginal	Neonatal	2	C	NNU	Female	35-40	3200	BF	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422698	C01990	Mother	Vaginal	Vaginal	Mother	2	C	NA	Female	35-40	3200	NA	NA	NA	NA	no	Yes	no	Yes	NA	NA	2.2E+07	1.9E+07
ERS3422699	C01991	21	Vaginal	Vaginal	Neonatal	2	C	NNU	Female	35-40	2900	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2E+07	1.6E+07
ERS3422700	C01991	4	Vaginal	Vaginal	Neonatal	2	C	NNU	Female	35-40	2900	NoBF	No	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422701	C01991	7	Vaginal	Vaginal	Neonatal	2	C	NNU	Female	35-40	2900	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3422702	C01991	Mother	Vaginal	Vaginal	Mother	2	C	NA	Female	35-40	2900	NA	NA	NA	NA	no	Yes	no	Yes	NA	NA	1.8E+07	1.5E+07
ERS3422703	C01994	21	Vaginal	Vaginal	Neonatal	6	C	MCU	Female	40-45	3800	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422704	C01994	4	Vaginal	Vaginal	Neonatal	6	C	MCU	Female	40-45	3800	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.9E+07
ERS3422705	C01994	7	Vaginal	Vaginal	Neonatal	6	C	MCU	Female	40-45	3800	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.7E+07
ERS3422706	C01994	Mother	Vaginal	Vaginal	Mother	6	C	NA	Female	40-45	3800	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.2E+07	1.8E+07
ERS3422707	C01994	Infancy	Vaginal	Vaginal	9.33	6	C	MCU	Female	40-45	3800	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.8E+07	1.7E+07
ERS3422708	C02016	21	Caesarean	Elective_CS	Neonatal	3	C	Postnatal	Female	25-30	2800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.6E+07
ERS3422709	C02016	4	Caesarean	Elective_CS	Neonatal	3	C	Postnatal	Female	25-30	2800	NA	NA	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.4E+07
ERS3422710	C02016	7	Caesarean	Elective_CS	Neonatal	3	C	Postnatal	Female	25-30	2800	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3422711	C02044	4	Caesarean	Elective_CS	Neonatal	6	C	Postnatal	Male	35-40	3600	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.2E+07
ERS3422712	C02044	7	Caesarean	Elective_CS	Neonatal	6	C	Postnatal	Male	35-40	3600	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.4E+07
ERS3422713	C02044	Mother	Caesarean	Elective_CS	Mother	6	C	NA	Male	35-40	3600	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.1E+07	1.7E+07
ERS3422714	C02044	21	Caesarean	Elective_CS	Neonatal	6	C	Postnatal	Male	35-40	3600	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.3E+07
ERS3422715	C02047	21	Caesarean	Emergency_	Neonatal	3	C	MCU	Male	35-40	3700	Mixed	Yes	No	Yes	no	No	no	Yes	NA	low_Bacteroides	2.1E+07	1.7E+07
ERS3422716	C02047	4	Caesarean	Emergency_	Neonatal	3	C	MCU	Male	35-40	3700	Mixed	Yes	No	Yes	no	No	no	Yes	NA	low_Bacteroides	1.8E+07	1.5E+07
ERS3422717	C02047	7	Caesarean	Emergency_	Neonatal	3	C	MCU	Male	35-40	3700	Mixed	Yes	No	Yes	no	No	no	Yes	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422718	C02047	Mother	Caesarean	Emergency_	Mother	3	C	NA	Male	35-40	3700	NA	NA	NA	Yes	no	No	no	Yes	NA	NA	2.6E+07	2.2E+07
ERS3422719	C02056	21	Caesarean	Elective_CS	Neonatal	2	C	Postnatal	NA	25-30	3200	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	3.5E+07	3.1E+07
ERS3422720	C02056	7	Caesarean	Elective_CS	Neonatal	2	C	Postnatal	NA	25-30	3200	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422721	C02056	Mother	Caesarean	Elective_CS	Mother	2	C	NA	NA	25-30	3200	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2E+07	1.7E+07
ERS3422722	C02056	Infancy	Caesarean	Elective_CS	8.57	2	C	Postnatal	NA	25-30	3200	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422723	C02057	7	Caesarean	Emergency_	Neonatal	NA	C	NA	NA	30-35	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3422724	C02057	21	Caesarean	Emergency_	Neonatal	NA	C	NA	NA	30-35	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	3E+07	2.7E+07
ERS3422725	C02057	4	Caesarean	Emergency_	Neonatal	NA	C	NA	NA	30-35	NA	Mixed	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422726	C02057	Mother	Caesarean	Emergency_	Mother	NA	C	NA	NA	30-35	NA	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2E+07	1.7E+07
ERS3422727	C02058	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	35-40	2900	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.3E+07	2E+07
ERS3422728	C02058	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	35-40	2900	Mixed	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422729	C02058	21	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	35-40	2900	Mixed	Yes	No	NA	no	Yes	no	No	NA	low_Bacteroides	2.1E+07	1.9E+07
ERS3422730	C02059	21	Caesarean	Elective_CS	Neonatal	4	C	MCU	Female	35-40	3300	Mixed	Yes	Yes	Yes	no	NA	Yes	No	Yes	low_Bacteroides	1.8E+07	1.5E+07
ERS3422731	C02059	4	Caesarean	Elective_CS	Neonatal	4	C	MCU	Female	35-40	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.2E+07
ERS3422732	C02059	7	Caesarean	Elective_CS	Neonatal	4	C	MCU	Female	35-40	3300	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	2.3E+07	2E+07
ERS3422733	C02059	Mother	Caesarean	Elective_CS	Mother	4	C	NA	Female	35-40	3300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.1E+07	1.8E+07
ERS3422738	C02061	21	Vaginal	Vaginal	Neonatal	1	C	MCU	Male	35-40	3600	BF	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.6E+07	2.1E+07
ERS3422739	C02061	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	35-40	3600	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3422740	C02061	Infancy	Vaginal	Vaginal	8.50	1	C	MCU	Male	35-40	3600	Mixed	Yes	No	NA	no	NA	no	No	No	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422741	C02061	4	Vaginal	Vaginal	Neonatal	1	C	MCU	Male	35-40	3600	Mixed	Yes	No	NA	no	NA	no	No	NA	normal_Bacteroides	1.5E+07	1.3E+07
ERS3422742	C02062	21	Vaginal	Vaginal	Neonatal	3	C	MCU	Male	35-40	2500	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	normal_Bacteroides	2.3E+07	1.9E+07
ERS3422743	C02062	4	Vaginal	Vaginal	Neonatal	3	C	MCU	Male	35-40	2500	BF	Yes	No	NA	no	Yes	no	Yes	NA	normal_Bacteroides	2.1E+07	1.7E+07
ERS3422744	C02062	7	Vaginal	Vaginal	Neonatal	3	C	MCU	Male	35-40	2500	BF	Yes	No	NA	no	Yes	no	Yes	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422745	C02062	Infancy	Vaginal	Vaginal	8.30	3	C	MCU	Male	35-40	2500	NA	NA	No	NA	no	Yes	no	Yes	NA	normal_Bacteroides	2.7E+07	2.3E+07
ERS3422746	C02097	Mother	Vaginal	Vaginal	Mother	2	C	NA	Female	40-45	2300	NA	NA	NA	NA	no	Yes	no	Yes	NA	NA	3.2E+07	2.7E+07
ERS3422747	C02097	21	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Female	40-45	2300	BF	Yes	Yes	NA	no	Yes	no	Yes	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3422748	C02097	7	Vaginal	Vaginal	Neonatal	2	C	Postnatal	Female	40-45	2300	BF	Yes	Yes	NA	no	Yes	no	Yes	NA	low_Bacteroides	1.9E+07	1.5E+07
ERS3422749	C02130	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Male	35-40	2900	BF	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422750	C02130	Infancy	Vaginal	Vaginal	7.93	1	C	MCU	Male	35-40	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2E+07	1.8E+07
ERS3422751	C02131	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Male	30-35	3500	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422752	C02131	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	30-35	3500	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.5E+07	2.1E+07
ERS3422734	C02131	Infancy	Vaginal	Vaginal	8.57	1	C	Postnatal	Male	30-35	3500	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.8E+07
ERS3422735	C02142	7	Caesarean	Elective_CS	Neonatal	1	C	NA	Female	30-35	3300	BF	Yes	NA	Yes	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.7E+07

ERS3422736	C02142	Mother	Caesarean	Elective_CS	Mother	1	C	NA	Female	30-35	3300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.5E+07	2.2E+07
ERS3422737	C02143	7	Vaginal	Vaginal	Neonatal	0	C	NA	Female	25-30	3200	BF	Yes	NA	NA	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.1E+07
ERS3422753	C02143	Mother	Vaginal	Vaginal	Mother	0	C	NA	Female	25-30	3200	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.1E+07	1.7E+07
ERS3422754	C02143	Infancy	Vaginal	Vaginal	7.77	0	C	NA	Female	25-30	3200	Mixed	Yes	NA	NA	no	NA	no	No	NA	low_Bacteroides	1.7E+07	1.5E+07
ERS3422755	C02180	7	Vaginal	Vaginal	Neonatal	1	C	NNU	Male	40-45	2500	Mixed	Yes	No	NA	no	Yes	no	Yes	NA	low_Bacteroides	3E+07	2.6E+07
ERS3422756	C02180	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	40-45	2500	NA	NA	NA	NA	no	Yes	no	Yes	NA	NA	2.9E+07	2.4E+07
ERS3422757	C02186	7	Vaginal	Vaginal	Neonatal	2	C	MCU	Male	30-35	3200	NA	NA	Yes	NA	no	Yes	no	No	NA	low_Bacteroides	2E+07	1.6E+07
ERS3422758	C02186	Mother	Vaginal	Vaginal	Mother	2	C	NA	Male	30-35	3200	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.5E+07	2.2E+07
ERS3422759	C02190	7	Caesarean	Elective_CS	Neonatal	1	C	MCU	Female	35-40	3500	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3422760	C02190	Infancy	Caesarean	Elective_CS	7.43	1	C	MCU	Female	35-40	3500	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.8E+07
ERS3422761	C02223_T1	7	Caesarean	Elective_CS	Neonatal	4	C	TC	Male	NA	2300	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.3E+07	1.8E+07
ERS3422762	C02223_T2	7	Caesarean	Elective_CS	Neonatal	4	C	TC	Male	NA	2300	Mixed	Yes	No	Yes	no	NA	no	Yes	No	low_Bacteroides	2E+07	1.6E+07
ERS3422763	C02223	Mother	Caesarean	Elective_CS	Mother	4	C	NA	Male	30-35	2300	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.2E+07	1.9E+07
ERS3422764	C02223_T1	Infancy	Caesarean	Elective_CS	7.40	4	C	TC	Male	NA	2300	BF	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3422765	C02223_T2	Infancy	Caesarean	Elective_CS	7.40	4	C	TC	Male	NA	2300	Mixed	Yes	No	Yes	no	NA	no	Yes	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3422766	C02236	7	Caesarean	Emergency_	Neonatal	2	C	Postnatal	Male	30-35	3800	BF	Yes	No	Yes	no	No	no	No	No	low_Bacteroides	2.7E+07	2.3E+07
ERS3422767	C02236	Mother	Caesarean	Emergency_	Mother	2	C	NA	Male	30-35	3800	NA	NA	NA	Yes	no	No	no	NA	NA	NA	2.5E+07	2.1E+07
ERS3422768	C02236	Infancy	Caesarean	Emergency_	7.67	2	C	Postnatal	Male	30-35	3800	Mixed	Yes	No	Yes	no	No	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422769	C02294_T1	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	NA	2400	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.2E+07	1.8E+07
ERS3422770	C02294_T2	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	NA	2400	BF	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.7E+07	2.3E+07
ERS3422771	C02294	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	30-35	2400	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2E+07	1.7E+07
ERS3422772	C02295	7	Caesarean	Elective_CS	Neonatal	1	C	MCU	Female	40-45	2700	BF	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.6E+07	2.2E+07
ERS3422773	C02295	Mother	Caesarean	Elective_CS	Mother	1	C	NA	Female	40-45	2700	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3422774	C02295	Infancy	Caesarean	Elective_CS	8.87	1	C	MCU	Female	40-45	2700	Mixed	Yes	No	Yes	no	NA	no	No	NA	low_Bacteroides	2.5E+07	2.3E+07
ERS3422775	C02323	7	Caesarean	Elective_CS	Neonatal	1	C	MCU	Female	30-35	2900	BF	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	1.9E+07	1.7E+07
ERS3422776	C02323	Infancy	Caesarean	Elective_CS	7.27	1	C	MCU	Female	30-35	2900	Mixed	Yes	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.9E+07	1.7E+07
ERS3422777	C02331	7	Vaginal	Vaginal	Neonatal	2	C	MCU	Female	25-30	2500	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	1.8E+07	1.5E+07
ERS3422778	C02331	Mother	Vaginal	Vaginal	Mother	2	C	NA	Female	25-30	2500	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.3E+07	1.9E+07
ERS3422779	C02345	7	Caesarean	Elective_CS	Neonatal	1	C	MCU	Female	25-30	3400	NoBF	No	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.5E+07	2.3E+07
ERS3422780	C02345	Infancy	Caesarean	Elective_CS	7.37	1	C	MCU	Female	25-30	3400	NoBF	No	Yes	Yes	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422781	C02353	Mother	Vaginal	Vaginal	Mother	0	C	NA	Female	35-40	3600	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.5E+07	2.1E+07
ERS3422782	C02353	7	Vaginal	Vaginal	Neonatal	0	C	MCU	Female	35-40	3600	NA	NA	No	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422783	C02377	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Female	45-50	3500	Mixed	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	2E+07
ERS3422784	C02377	Infancy	Vaginal	Vaginal	6.57	1	C	MCU	Female	45-50	3500	NA	NA	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.2E+07	1.8E+07
ERS3422785	C02391	Mother	Vaginal	Vaginal	Mother	1	C	NA	Female	30-35	3600	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.3E+07	1.9E+07
ERS3422786	C02391	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Female	30-35	3600	BF	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.1E+07	1.6E+07
ERS3422787	C02391	Infancy	Vaginal	Vaginal	7.13	1	C	MCU	Female	30-35	3600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422788	C02406	7	Vaginal	Vaginal	Neonatal	0	C	MCU	Female	40-45	4000	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2.3E+07	2E+07
ERS3422789	C02406	Infancy	Vaginal	Vaginal	6.27	0	C	MCU	Female	40-45	4000	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	2.1E+07	1.8E+07
ERS3422790	C02411	Infancy	Vaginal	Vaginal	6.80	1	C	Postnatal	Female	35-40	3400	Mixed	Yes	Yes	NA	no	Yes	no	No	NA	normal_Bacteroides	2.3E+07	2.1E+07
ERS3422791	C02411	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	35-40	3400	Mixed	Yes	Yes	NA	no	Yes	no	No	No	normal_Bacteroides	2E+07	1.8E+07
ERS3422792	C02438	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	30-35	2600	BF	Yes	Yes	NA	no	NA	no	No	No	normal_Bacteroides	2E+07	1.8E+07
ERS3422793	C02438	Infancy	Vaginal	Vaginal	4.67	1	C	Postnatal	Female	30-35	2600	Mixed	Yes	Yes	NA	no	NA	no	No	NA	normal_Bacteroides	1.7E+07	1.5E+07
ERS3422794	C02471	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	30-35	3200	Mixed	Yes	No	NA	no	Yes	no	No	NA	normal_Bacteroides	1.9E+07	1.6E+07
ERS3422795	C02471	Infancy	Vaginal	Vaginal	5.93	1	C	Postnatal	Female	30-35	3200	Mixed	Yes	No	NA	no	Yes	no	No	NA	normal_Bacteroides	3.9E+07	3.4E+07
ERS3422796	C02497	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Male	25-30	3400	Mixed	Yes	No	NA	no	Yes	no	No	No	low_Bacteroides	2.2E+07	2E+07
ERS3422797	C02497	Infancy	Vaginal	Vaginal	5.97	1	C	MCU	Male	25-30	3400	Mixed	Yes	No	NA	no	Yes	no	No	No	low_Bacteroides	1.7E+07	1.5E+07
ERS3422798	C02514	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	30-35	3400	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3422799	C02514	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Male	30-35	3400	BF	Yes	Yes	NA	no	NA	no	No	Yes	low_Bacteroides	2.1E+07	1.7E+07
ERS3422800	C02514	Infancy	Vaginal	Vaginal	5.80	1	C	MCU	Male	30-35	3400	Mixed	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3422801	C02516	Mother	Vaginal	Vaginal	Mother	3	C	NA	Female	35-40	2800	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.4E+07	2E+07
ERS3422802	C02516	7	Vaginal	Vaginal	Neonatal	3	C	MCU	Female	35-40	2800	Mixed	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2E+07	1.6E+07
ERS3422803	C02516	Infancy	Vaginal	Vaginal	6.33	3	C	MCU	Female	35-40	2800	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	1.6E+07	1.4E+07
ERS3422804	C02526	7	Vaginal	Vaginal	Neonatal	1	C	Postnatal	Female	30-35	3100	BF	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	1.8E+07	1.6E+07
ERS3422805	C02526	Infancy	Vaginal	Vaginal	7.83	1	C	Postnatal	Female	30-35	3100	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	1.8E+07	1.6E+07
ERS3422806	C02548	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	35-40	3800	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.5E+07	2.2E+07
ERS3422807	C02548	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Male	35-40	3800	BF	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.3E+07	1.9E+07
ERS3422808	C02552	Infancy	Vaginal	Vaginal	5.63	4	C	Postnatal	Female	35-40	3300	Mixed	Yes	No	NA	no	NA	no	No	NA	low_Bacteroides	2.4E+07	2.1E+07
ERS3422809	C02552	7	Vaginal	Vaginal	Neonatal	4	C	Postnatal	Female	35-40	3300	BF	Yes	No	NA	no	NA	no	No	No	low_Bacteroides	2E+07	1.7E+07
ERS3422810	C02565	Mother	Caesarean	Elective_CS	Mother	2	C	NA	Male	35-40	3400	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.3E+07	2E+07
ERS3422811	C02565	7	Caesarean	Elective_CS	Neonatal	2	C	COB	Male	35-40	3400	Mixed	Yes	No	Yes	no	NA	no	No	No	low_Bacteroides	2.4E+07	1.9E+07
ERS3422812	C02566	Mother	Caesarean	Emergency_	Mother	4	C	NA	Male	35-40	3000	NA	NA	NA	Yes	no	No	no	NA	NA	NA	2.7E+07	2.3E+07
ERS3422813	C02566	7	Caesarean	Emergency_	Neonatal	4	C	MCU	Male	35-40	3000	Mixed	Yes	No	Yes	no	No	no	No	No	low_Bacteroides	3E+07	2.5E+07
ERS3422814	C02571	Mother	Vaginal	Vaginal	Mother	3	C	NA	Male	30-35	3500	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.5E+07	2.1E+07
ERS3422815	C02571	7	Vaginal	Vaginal	Neonatal	3	C	MCU	Male	30-35	3500	BF	Yes	No	NA	no	NA	Yes	No	Yes	normal_Bacteroides	2.1E+07	1.7E+07
ERS3422816	C02634	Mother	Vaginal	Vaginal	Mother	3	C	NA	Male	30-35	3000	NA	NA	NA	NA	no	Yes	no	NA	NA	NA	2.5E+07	2.1E+07
ERS3422817	C02634	7	Vaginal	Vaginal	Neonatal	3	C	Postnatal	Male	30-35	3000	BF	Yes	Yes	NA	no	Yes	no	No	No	low_Bacteroides	2.4E+07	1.9E+07
ERS3422818	C02649	7	Vaginal	Vaginal	Neonatal	1	C	MCU	Male	30-35	3600	Mixed	Yes	Yes	NA	no	NA	no	No	No	low_Bacteroides	2.3E+07	1.8E+07
ERS3422819	C02649	Mother	Vaginal	Vaginal	Mother	1	C	NA	Male	30-35	3600	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.7E+07	2.3E+07
ERS3422820	C02670	7	Caesarean	Emergency_	Neonatal	2	C	MCU	Female	35-40	3500	BF	Yes	No	Yes	no	No	no	No	No	low_Bacteroides	2.2E+07	1.7E+07
ERS3422821	C02670	Mother	Caesarean	Emergency_	Mother	2	C	NA	Female	35-40	3500	NA	NA	NA	Yes	no	No	no	NA	NA	NA	2.4E+07	1.9E+07
ERS3422822	C02695	Mother	Vaginal	Vaginal	Mother	2	C	NA	Female	30-35	2900	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.1E+07	1.8E+07
ERS3422823	C02695	7	Vaginal	Vaginal	Neonatal	2	C	MCU	Female	30-35	2900	Mixed	Yes	Yes	NA	no	NA	no	No	NA	low_Bacteroides	2.1E+07	1.6E+07
ERS3422824	C02755	Mother	Vaginal	Vaginal	Mother	5	C	NA	Male	35-40	3100	NA	NA	NA	NA	no	NA	no	Yes	NA	NA	2.5E+07	2.1E+07
ERS3422825	C02755	7	Vaginal	Vaginal	Neonatal	5	C	MCU	Male	35-40	3100	Mixed	Yes	No	NA	no	NA	no	Yes	Yes	low_Bacteroides	1.9E+07	1.4E+07
ERS3422826	C02756	Mother	Caesarean	Elective_CS	Mother	3	C	NA	Female	40-45	2900	NA	NA	NA	Yes	no	NA	no	NA	NA	NA	2.4E+07	2.1E+07
ERS3422827	C02756	7	Caesarean	Elective_CS	Neonatal	3	C	Postnatal	Female	40-45	2900	Mixed	Yes	Yes	Yes	no	NA	no	No	No	low_Bacteroides	2.8E+07	2.4E+07
ERS3422828	C02868	Mother	Caesarean	Emergency_	Mother	1	C	NA	Male	35-40	3700	NA	NA	NA	Yes	no	No	no	NA	NA	NA	2.2E+07	1.8E+07
ERS3422829	C02868	7	Caesarean	Emergency_	Neonatal	1	C	MCU	Male	35-40	3700	Mixed	Yes	Yes	Yes	no	No	no	No	No	low_Bacteroides	6848100	5014038
ERS3422830	C02892	7	Vaginal	Vaginal	Neonatal	2	C	MCU	Male	35-40	4200	Mixed	Yes	Yes	NA	no	NA	Yes	No	Yes	low_Bacteroides	2.4E+07	2E+07
ERS3422831	C02892	Mother	Vaginal	Vaginal	Mother	2	C	NA	Male	35-40	4200	NA	NA	NA	NA	no	NA	no	NA	NA	NA	2.5E+07	2.2E+07
ERS3422832	C_Fresh_01	7	Caesarean	Elective_CS	Neonatal	NA	C	NA	NA	NA	NA	BF	Yes	NA	Yes	no	NA	no	NA	NA	low_Bacteroides	2.8E+07	2.5E+07

Appendix 3 Summary of early maternal strain transmissions

Transmission events in 178 mother-baby pairs with early (neonatal) transmission events counted at least once. Most frequently shared bacterial species countable for early transmission analysis shown in Figure 2.12 are highlighted in bold (more than 10 countable mother-neonatal sample pairs). Opportunistic pathogens are highlighted in red. Where applicable species names are updated according to the latest curation in the GTDB (release 03-RS86, http://gtdb.ecogenomic.org) by querying the reference genomes used in the metaphlan2 database (original metaphlan2 species names in brackets).

Species available for strain profiling	Vaginal				Caesarean section				Total transmissions			Total countable		
	Early		Late		Early		Late		Early	Late	All	Early	Late	All
	Yes	No	Yes	No	Yes	No	Yes	No						
Bifidobacterium longum	39	7	6	17	7	5	7	10	46	13	59	58	40	98
Escherichia coli	27	14	5	10	9	7	8	9	36	13	49	57	32	89
Streptococcus salivarius	2	42	0	8	2	22	1	5	4	1	5	68	14	82
Bacteroides uniformis	31	3	9	2	1	2	2	0	32	11	43	37	13	50
Parabacteroides distasonis	31	0	10	0	0	0	2	0	31	12	43	31	12	43
Bacteroides vulgatus	25	6	6	2	2	1	1	0	27	7	34	34	9	43
Streptococcus thermophilus	1	17	3	3	0	15	1	2	1	4	5	33	9	42
Bifidobacterium bifidum	24	1	10	0	2	0	3	1	26	13	39	27	14	41
Collinsella aerofaciens	17	4	8	0	2	0	0	3	19	8	27	23	11	34
Bacteroides dorei	21	0	9	0	1	0	1	0	22	10	32	22	10	32
Bacteroides xylanisolvens (Bacteroides_sp_2_1_22)	16	1	9	1	0	0	1	0	16	10	26	17	11	28
Ruminococcus torques	0	5	4	5	1	1	4	5	1	8	9	7	18	25
Bacteroides fragilis	12	0	6	1	2	0	3	0	14	9	23	14	10	24
Blautia wexlerae (Ruminococcus_sp_5_1_39BFAA)	1	0	5	6	2	0	7	2	3	12	15	3	20	23
Bifidobacterium pseudocatenulatum	13	0	4	0	4	0	1	0	17	5	22	17	5	22
Parabacteroides merdae	14	0	6	0	0	0	1	0	14	7	21	14	7	21
Bacteroides ovatus	11	0	5	1	1	0	2	0	12	7	19	12	8	20
Streptococcus vestibularis	3	6	0	1	3	6	0	1	6	0	6	18	2	20
Bifidobacterium adolescentis	12	4	0	1	0	0	2	0	12	2	14	16	3	19
Bacteroides thetaiotaomicron	11	1	3	0	1	0	0	0	12	3	15	13	3	16
Faecalibacterium prausnitzii	0	0	1	9	0	0	0	6	0	1	1	0	16	16
Bacteroides caccae	5	0	7	0	0	0	0	0	5	7	12	5	7	12
Streptococcus parasanguinis	0	6	0	0	1	5	0	0	1	0	1	12	0	12
Enterococcus faecalis	2	0	0	0	4	3	1	1	6	1	7	9	2	11
Bifidobacterium catenulatum	7	0	3	0	0	0	0	0	7	3	10	7	3	10
Bacteroides stercoris	7	0	1	0	0	0	0	0	7	1	8	7	1	8
Ruminococcus gnavus	2	1	3	0	0	0	0	2	2	3	5	3	5	8
Bacteroides faecis	4	0	3	0	0	0	0	0	4	3	7	4	3	7
Clostridium bartlettii	4	0	0	0	1	0	2	0	5	2	7	5	2	7
Alistipes onderdonkii	3	0	1	0	0	0	1	1	3	2	5	3	3	6
Eggerthella lenta (Eggerthella_sp_1_3_56FAA)	3	0	0	0	1	1	0	1	4	0	4	5	1	6
Bifidobacterium breve	2	1	1	0	1	0	1	0	3	2	5	4	2	6
Enterococcus faecium	1	1	0	1	1	1	0	0	2	0	2	4	1	5
Eubacterium eligens	1	0	1	1	0	0	0	2	1	1	2	1	4	5
Streptococcus sp3 (Streptococcus_sp_C150)	1	1	0	1	0	2	0	0	1	0	1	4	1	5
Akkermansia muciniphila	0	0	2	1	0	0	2	0	0	4	4	0	5	5
Eubacterium rectale	0	0	0	2	0	0	1	2	0	1	1	0	5	5

Species available for strain profiling	Vaginal				Caesarean section				Total transmissions			Total countable		
	Early		Late		Early		Late		Early	Late	All	Early	Late	All
	Yes	No	Yes	No	Yes	No	Yes	No						
Sutterella wadsworthensis	4	0	0	0	0	0	0	0	4	0	4	4	0	4
Bacteroides massiliensis	3	0	1	0	0	0	0	0	3	1	4	3	1	4
Eubacterium biforme	3	1	0	0	0	0	0	0	3	0	3	4	0	4
Bacteroides cellulosilyticus	2	0	0	0	1	0	1	0	3	1	4	3	1	4
Ruminococcus obeum	1	0	0	2	0	1	0	0	1	0	1	2	2	4
Eubacterium hallii	0	0	2	1	0	0	0	1	0	2	2	0	4	4
Haemophilus parainfluenzae	0	1	0	1	0	2	0	0	0	0	0	3	1	4
Odoribacter splanchnicus	1	0	1	1	0	0	0	0	1	1	2	1	2	3
Barnesiella intestinihominis	0	0	2	0	0	0	1	0	0	3	3	0	3	3
Dorea formicigenerans	0	0	1	0	0	0	2	0	0	3	3	0	3	3
Dorea longicatena	0	0	2	1	0	0	0	0	0	2	2	0	3	3
Klebsiella oxytoca	0	1	0	0	2	0	0	0	2	0	2	3	0	3
Ruminococcus bromii	0	0	0	1	0	0	0	2	0	0	0	0	3	3
Coprobacter fastidiosus	2	0	0	0	0	0	0	0	2	0	2	2	0	2
Bifidobacterium angulatum	2	0	0	0	0	0	0	0	2	0	2	2	0	2
Citrobacter freundii	1	0	0	1	0	0	0	0	1	0	1	1	1	2
Parabacteroides johnsonii	1	0	1	0	0	0	0	0	1	1	2	1	1	2
Alistipes finegoldii (Alistipes_sp_HGB5)	0	0	1	0	0	0	1	0	0	2	2	0	2	2
Clostridium ramosum	0	0	1	0	0	0	1	0	0	2	2	0	2	2
Klebsiella pneumoniae	0	0	0	1	1	0	0	0	1	0	1	1	1	2
Roseburia inulinivorans	0	0	1	0	0	0	0	1	0	1	1	0	2	2
Alistipes putredinis	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Bacteroides coprophilus	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Bacteroides eggerthii	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Clostridium bolteae	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Eubacterium D innocuum (Erysipelotrichaceae_bacterium_6_1_45)	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Lactobacillus gasseri	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Roseburia hominis	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Staphylococcus epidermidis	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Streptococcus australis	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Ruthenibacterium lactatiformans (Subdoligranulum_sp_4_3_54A2FAA)	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Alistipes shahii	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Bifidobacterium animalis	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Citrobacter koseri	0	0	0	0	1	0	0	0	1	0	1	1	0	1
Clostridium nexile	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Coprobacillus cateniformis (Coprobacillus_sp_29_1)	0	0	0	0	0	0	1	0	0	1	1	0	1	1

Species available for strain profiling	Vaginal				Caesarean section				Total transmissions			Total countable		
	Early		Late		Early		Late		Early	Late	All	Early	Late	All
	Yes	No	Yes	No	Yes	No	Yes	No						
Coprococcus comes	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Coprococcus eutactus (Coprococcus_sp_ART55_1)	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Enterobacter cloacae	0	0	0	0	1	0	0	0	1	0	1	1	0	1
Enterococcus durans	0	0	0	0	0	0	1	0	0	1	1	0	1	1
Eubacterium ramulus	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Lactobacillus fermentum	0	0	0	0	0	0	1	0	0	1	1	0	1	1
Lactobacillus rhamnosus	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Lactococcus lactis	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Oscillibacter sp6 (Oscillibacter_sp_KLE_1745)	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Roseburia intestinalis	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Ruminococcus callidus	0	0	0	0	0	0	1	0	0	1	1	0	1	1
Ruminococcus lactaris	0	1	0	0	0	0	0	0	0	0	0	1	0	1

Appendix 4 Summary of early and late maternal strain transmissions

Transmission events in 59 mother-baby pairs with both early (neonatal) and late (infancy) transmission events counted. Most frequently shared bacterial species countable for early transmission analysis shown in Figure 2.13a are highlighted in bold (more than 10 countable mother-neonatal sample pairs). Opportunistic pathogens are highlighted in red. Where applicable species names are updated according to the latest curation in the GTDB (release 03-RS86, http://gtdb.ecogenomic.org) by querying the reference genomes used in the metaphlan2 database (original metaphlan2 species names in brackets)

Species available for strain profiling	Vaginal				C-section				Total transmissions			Total countable		
	Early		Late		Early		Late		Early	Late	All	Early	Late	All
	Yes	No	Yes	No	Yes	No	Yes	No						
Bifidobacterium longum	11	1	6	17	1	4	7	10	12	13	25	17	40	57
Escherichia coli	11	3	5	10	6	2	8	9	17	13	30	22	32	54
Streptococcus salivarius	0	14	0	8	1	8	1	5	1	1	2	23	14	37
Bacteroides uniformis	13	0	9	2	0	0	2	0	13	11	24	13	13	26
Bifidobacterium bifidum	9	0	10	0	1	0	3	1	10	13	23	10	14	24
Parabacteroides distasonis	12	0	10	0	0	0	2	0	12	12	24	12	12	24
Ruminococcus torques	0	4	4	5	1	1	4	5	1	8	9	6	18	24
Streptococcus thermophilus	1	6	3	3	0	5	1	2	1	4	5	12	9	21
Bacteroides vulgatus	8	2	6	2	0	1	1	0	8	7	15	11	9	20
Blautia wexlerae (Ruminococcus sp 5 1 39BFAA)	0	0	5	6	0	0	7	2	0	12	12	0	20	20
Bacteroides xylanisolvens (Bacteroides_sp_2_1_22)	8	0	9	1	0	0	1	0	8	10	18	8	11	19
Collinsella aerofaciens	6	2	8	0	0	0	0	3	6	8	14	8	11	19
Bacteroides dorei	7	0	9	0	0	0	1	0	7	10	17	7	10	17
Bacteroides fragilis	6	0	6	1	1	0	3	0	7	9	16	7	10	17
Faecalibacterium prausnitzii	0	0	1	9	0	0	0	6	0	1	1	0	16	16
Bacteroides ovatus	5	0	5	1	0	0	2	0	5	7	12	5	8	13
Bifidobacterium pseudocatenulatum	5	0	4	0	1	0	1	0	6	5	11	6	5	11
Parabacteroides merdae	4	0	6	0	0	0	1	0	4	7	11	4	7	11
Bacteroides caccae	3	0	7	0	0	0	0	0	3	7	10	3	7	10
Bifidobacterium adolescentis	4	2	0	1	0	0	2	0	4	2	6	6	3	9
Ruminococcus gnavus	2	0	3	0	0	0	0	2	2	3	5	2	5	7
Streptococcus vestibularis	0	4	0	1	0	1	0	1	0	0	0	5	2	7
Bacteroides faecis	1	2	3	0	0	0	0	0	1	3	4	3	3	6
Bacteroides thetaiotaomicron	3	0	3	0	0	0	0	0	3	3	6	3	3	6
Bifidobacterium catenulatum	0	3	3	0	0	0	0	0	0	3	3	3	3	6
Enterococcus faecalis	2	0	0	0	1	1	1	1	3	1	4	4	2	6
Akkermansia muciniphila	0	0	2	1	0	0	2	0	0	4	4	0	5	5
Eubacterium rectale	0	0	0	2	0	0	1	2	0	1	1	0	5	5
Alistipes onderdonkii	1	0	1	0	0	0	1	1	1	2	3	1	3	4
Bifidobacterium breve	1	0	1	0	1	0	1	0	2	2	4	2	2	4
Eubacterium eligens	0	0	1	1	0	0	0	2	0	1	1	0	4	4
Eubacterium hallii	0	0	2	1	0	0	0	1	0	2	2	0	4	4
Barnesiella intestinihominis	0	0	2	0	0	0	1	0	0	3	3	0	3	3
Clostridium bartlettii	1	0	0	0	0	0	2	0	1	2	3	1	2	3
Dorea formicigenerans	0	0	1	0	0	0	2	0	0	3	3	0	3	3
Dorea longicatena	0	0	2	1	0	0	0	0	0	2	2	0	3	3
Enterococcus faecium	0	1	0	1	1	0	0	0	1	0	1	2	1	3

Species available for strain profiling	Vaginal				C-section				Total transmissions			Total countable		
	Early		Late		Early		Late		Early	Late	All	Early	Late	All
	Yes	No	Yes	No	Yes	No	Yes	No						
Ruminococcus bromii	0	0	0	1	0	0	0	2	0	0	0	0	3	3
Ruminococcus obeum	1	0	0	2	0	0	0	0	1	0	1	1	2	3
Streptococcus parasanguinis	0	2	0	0	0	1	0	0	0	0	0	3	0	3
Alistipes finegoldii (Alistipes_sp_HGB5)	0	0	1	0	0	0	1	0	0	2	2	0	2	2
Bacteroides cellulosilyticus	0	0	0	0	1	0	1	0	1	1	2	1	1	2
Bacteroides massiliensis	1	0	1	0	0	0	0	0	1	1	2	1	1	2
Citrobacter freundii	1	0	0	1	0	0	0	0	1	0	1	1	1	2
Clostridium ramosum	0	0	1	0	0	0	1	0	0	2	2	0	2	2
Eggerthella lenta (Eggerthella_sp_1_3_56FAA)	0	0	0	0	0	0	2	0	0	2	2	0	2	2
Eubacterium biforme	1	1	0	0	0	0	0	0	1	0	1	2	0	2
Haemophilus parainfluenzae	0	0	0	1	0	1	0	0	0	0	0	1	1	2
Klebsiella oxytoca	0	0	0	0	2	0	0	0	2	0	2	2	0	2
Odoribacter splanchnicus	0	0	1	1	0	0	0	0	0	1	1	0	2	2
Parabacteroides johnsonii	1	0	1	0	0	0	0	0	1	1	2	1	1	2
Roseburia inulinivorans	0	0	1	0	0	0	0	1	0	1	1	0	2	2
Coprobacter fastidiosus	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Alistipes putredinis	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Alistipes shahii	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Bacteroides stercoris	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Bifidobacterium animalis	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Citrobacter koseri	0	0	0	0	1	0	0	0	1	0	1	1	0	1
Clostridium bolteae	1	0	0	0	0	0	0	0	1	0	1	1	0	1
Clostridium nexile	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Coprobacillus cateniformis (Coprobacillus_sp_29_1)	0	0	0	0	0	0	1	0	0	1	1	0	1	1
Coprococcus comes	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Coprococcus eutactus (Coprococcus_sp_ART55_1)	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Enterococcus durans	0	0	0	0	0	0	1	0	0	1	1	0	1	1
Eubacterium ramulus	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Klebsiella pneumoniae	0	0	0	1	0	0	0	0	0	0	0	0	1	1
Lactobacillus fermentum	0	0	0	0	0	0	1	0	0	1	1	0	1	1
Lactobacillus rhamnosus	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Lactococcus lactis	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Oscillibacter sp6 (Oscillibacter_sp_KLE_1745)	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Roseburia intestinalis	0	0	1	0	0	0	0	0	0	1	1	0	1	1
Ruminococcus callidus	0	0	0	0	0	0	1	0	0	1	1	0	1	1
Ruminococcus lactaris	0	1	0	0	0	0	0	0	0	0	0	1	0	1

Species available for strain profiling	Vaginal				C-section				Total transmissions			Total countable		
	Early		Late		Early		Late		Early	Late	All	Early	Late	All
	Yes	No	Yes	No	Yes	No	Yes	No						
Streptococcus sp3 (Streptococcus_sp_C150)	0	0	0	1	0	0	0	0	0	0	0	0	1	1

Appendix 5 Accessions and metadata of the WGS study isolates

Accessions and metadata of the 836 isolates cultivated and analysed in this work. The most up-to-date genome-based taxonomic assignment was determined based on GTDB taxonomy nomenclature using GTDB-tk v1.0.2, as described in 4.1.3.

Sample_ID	Subject_ID	Sample_timepoints	Taxonomy_group	GTDB taxonomy	MLST	Delivery_mode	Source	Hospital
ERS2046353	514124	514124_7	Acinetobacter lwoffii	s__Acinetobacter fasciculus		Vaginal	Neonatal	A
ERS2046349	514124	514124_7	Anaerostipes caccae	s__Anaerostipes caccae		Vaginal	Neonatal	A
ERS2046359	515126	515126_10	Bacillus simplex	s__Bacillus_X simplex		Vaginal	Neonatal	A
ERS2046339	S19	S19_7	Bifidobacterium adolescentis	s__Bifidobacterium adolescentis		Vaginal	Neonatal	A
ERS2046337	S19	S19_7	Bifidobacterium breve	s__Bifidobacterium breve		Vaginal	Neonatal	A
ERS2046338	S19	S19_7	Bifidobacterium longum	s__Bifidobacterium longum		Vaginal	Neonatal	A
ERS2178882	A00908	A00908_M	Citrobacter braakii	s__Citrobacter braakii		Caesarean	Mother	A
ERS2178884	A00908	A00908_M	Citrobacter braakii	s__Citrobacter braakii		Caesarean	Mother	A
ERS2178885	A00908	A00908_M	Citrobacter braakii	s__Citrobacter braakii		Caesarean	Mother	A
ERS2178883	A00908	A00908_M	Citrobacter freundii	s__Citrobacter braakii		Caesarean	Mother	A
ERS2295855	A01921	A01921_7	Citrobacter freundii	s__Citrobacter braakii		Vaginal	Neonatal	A
ERS2178851	B00268	B00268_21	Citrobacter freundii	s__Citrobacter freundii		Vaginal	Neonatal	B
ERS2179035	C01752	C01752_M	Citrobacter freundii	s__Citrobacter freundii		Vaginal	Mother	C
ERS2443964	A00021_T1	A00021_T1_21	Clostridium butyricum	s__Absiella innocuum		Caesarean	Neonatal	A
ERS2046356	515126	515126_10	Clostridium disporicum	g__Clostridium		Vaginal	Neonatal	A
ERS846589	512120	512120_9	Clostridium perfringens	s__Clostridium_P perfringens		Caesarean	Neonatal	A
ERS2046347	514124	514124_7	Clostridium perfringens	s__Absiella innocuum		Vaginal	Neonatal	A
ERS2046348	514124	514124_7	Clostridium perfringens	s__Erysipelatoclostridium ramosum		Vaginal	Neonatal	A
ERS846592	519128	519128_12	Clostridium perfringens	s__Clostridium_P perfringens		Caesarean	Neonatal	A
ERS2046346	521130	521130_10	Clostridium perfringens	s__Clostridium_P perfringens		Vaginal	Neonatal	A
ERS2443963	A00021_T1	A00021_T1_21	Clostridium perfringens	s__Clostridium butyricum		Caesarean	Neonatal	A
ERS2444025	A01082	A01082_21	Clostridium perfringens	s__Clostridium_P perfringens		Caesarean	Neonatal	A
ERS2443978	A01580	A01580_21	Clostridium perfringens	s__Clostridium tertium		Caesarean	Neonatal	A
ERS2443979	A01580	A01580_7	Clostridium perfringens	s__Clostridium tertium		Caesarean	Neonatal	A
ERS2443980	A01580	A01580_4	Clostridium perfringens	s__Clostridium tertium		Caesarean	Neonatal	A
ERS2443989	B00010	B00010_4	Clostridium perfringens	s__Clostridium_P perfringens		Caesarean	Neonatal	B
ERS2443998	B00268	B00268_4	Clostridium perfringens	s__Clostridium_P perfringens		Vaginal	Neonatal	B
ERS2444006	B02156	B02156_7	Clostridium perfringens	s__Absiella innocuum		Vaginal	Neonatal	B
ERS2444007	B02156	B02156_7	Clostridium perfringens	s__Absiella innocuum		Vaginal	Neonatal	B
ERS2444008	B02255	B02255_21	Clostridium perfringens	s__Clostridium_P perfringens		Caesarean	Neonatal	B
ERS2046476	S2	S2_7	Clostridium perfringens	s__Clostridium_P perfringens		Caesarean	Neonatal	A
ERS2444017	C01329	C01329_4	Clostridium perfringens	s__Clostridium_P perfringens		Caesarean	Neonatal	C
ERS2444018	C01329	C01329_7	Clostridium perfringens	s__Clostridium tertium		Caesarean	Neonatal	C
ERS2046357	515126	515126_10	Clostridium ramosum	s__Erysipelatoclostridium ramosum		Vaginal	Neonatal	A
ERS2443965	A00021_T1	A00021_T1_21	Clostridium ramosum	s__Blautia producta		Caesarean	Neonatal	A
ERS2046358	515126	515126_10	Clostridium spiroforme	s__Erysipelatoclostridium spiroforme		Vaginal	Neonatal	A
ERS2443962	A00021_T1	A00021_T1_21	Clostridium sporogenes	s__Clostridium paraputrificum		Caesarean	Neonatal	A
ERS2046352	514124	514124_7	Corynebacterium jeikeium	s__Corynebacterium propinquum		Vaginal	Neonatal	A
ERS2046350	514124	514124_7	Dorea longicatena	s__Faecalicatena gnavus		Vaginal	Neonatal	A
ERS2178531	A00106_T1	A00106_T1_21	Enterobacter cloacae complex	s__Enterobacter ludwigii	374	Vaginal	Neonatal	A
ERS2178533	A00106_T1	A00106_T1_21	Enterobacter cloacae complex	s__Enterobacter ludwigii	374	Vaginal	Neonatal	A
ERS2178534	A00106_T2	A00106_T2_21	Enterobacter cloacae complex	s__Enterobacter ludwigii	374	Vaginal	Neonatal	A
ERS2178535	A00106_T2	A00106_T2_21	Enterobacter cloacae complex	s__Enterobacter ludwigii	489	Vaginal	Neonatal	A
ERS2178546	A00908_T1	A00908_T1_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	268	Caesarean	Neonatal	A
ERS2178562	A00908_T1	A00908_T1_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	268	Caesarean	Neonatal	A
ERS2178563	A00908_T1	A00908_T1_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	268	Caesarean	Neonatal	A
ERS2295820	A01057	A01057_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	141	Caesarean	Neonatal	A
ERS2178891	A01082	A01082_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	158	Caesarean	Neonatal	A
ERS2295825	A01082	A01082_7	Enterobacter cloacae complex	s__Enterobacter kobei	56	Caesarean	Neonatal	A
ERS2178502	A01580	A01580_7	Enterobacter cloacae complex	s__Enterobacter nimipressuralis	526	Caesarean	Neonatal	A
ERS2444027	A01580	A01580_4	Enterobacter cloacae complex	s__Enterobacter nimipressuralis	526	Caesarean	Neonatal	A
ERS2178560	A01676	A01676_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	1015	Caesarean	Neonatal	A
ERS2444038	A01676	A01676_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	493~	Caesarean	Neonatal	A
ERS2178537	A01862	A01862_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	493~	Caesarean	Neonatal	A
ERS2178539	A01862	A01862_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	489	Caesarean	Neonatal	A
ERS2178780	B00002	B00002_7	Enterobacter cloacae complex	s__Enterobacter kobei	125	Caesarean	Neonatal	B
ERS2178781	B00002	B00002_7	Enterobacter cloacae complex	s__Enterobacter kobei	125	Caesarean	Neonatal	B
ERS2178782	B00002	B00002_7	Enterobacter cloacae complex	s__Enterobacter kobei	125	Caesarean	Neonatal	B
ERS2178905	B00053	B00053_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	145	Caesarean	Neonatal	B
ERS2178791	B00071	B00071_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	63	Caesarean	Neonatal	B
ERS2178792	B00071	B00071_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	63	Caesarean	Neonatal	B
ERS2178585	B00076	B00076_7	Enterobacter cloacae complex	s__Enterobacter nimipressuralis	997~	Caesarean	Neonatal	B
ERS2178586	B00076	B00076_7	Enterobacter cloacae complex	s__Enterobacter nimipressuralis	997~	Caesarean	Neonatal	B
ERS2444016	B00076	B00076_7	Enterobacter cloacae complex	s__Enterobacter nimipressuralis	997~	Caesarean	Neonatal	B
ERS2178701	B00088	B00088_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	286	Caesarean	Neonatal	B
ERS2295760	B00092	B00092_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	145	Caesarean	Neonatal	B
ERS2178797	B00096	B00096_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	145	Caesarean	Neonatal	B
ERS2178802	B00096	B00096_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	145	Caesarean	Neonatal	B
ERS2178704	B00097	B00097_4	Enterobacter cloacae complex	s__Enterobacter cloacae_M	24~	Vaginal	Neonatal	B
ERS2178818	B00119	B00119_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	138	Vaginal	Neonatal	B
ERS2178820	B00119	B00119_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	138	Vaginal	Neonatal	B
ERS2295766	B00139	B00139_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	104	Caesarean	Neonatal	B
ERS2178568	B00174	B00174_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	145~	Caesarean	Neonatal	B
ERS2178569	B00174	B00174_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	145	Caesarean	Neonatal	B
ERS2178839	B00236	B00236_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	168	Vaginal	Neonatal	B
ERS2178918	B00268	B00268_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	310	Vaginal	Neonatal	B
ERS2178919	B00268	B00268_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	310	Vaginal	Neonatal	B
ERS2178920	B00268	B00268_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	310	Vaginal	Neonatal	B
ERS2178952	B01375	B01375_21	Enterobacter cloacae complex	s__Enterobacter bugandensis	1304~	Vaginal	Neonatal	B
ERS2178735	B02255	B02255_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	145~	Caesarean	Neonatal	B
ERS2178736	B02255	B02255_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	145	Caesarean	Neonatal	B
ERS2179016	C01331	C01331_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	145	Caesarean	Neonatal	C
ERS2179022	C01392	C01392_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	106	Caesarean	Neonatal	C
ERS2178506	C01689	C01689_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	336	Caesarean	Neonatal	C
ERS2179038	C01752	C01752_M	Enterobacter cloacae complex	s__Enterobacter himalayensis	286	Vaginal	Mother	C
ERS2295772	C01757	C01757_4	Enterobacter cloacae complex	s__Enterobacter himalayensis	104	Caesarean	Neonatal	C
ERS2429132	C01990	C01990_21	Enterobacter cloacae complex	s__Enterobacter himalayensis	346	Vaginal	Neonatal	C
ERS2429143	C02047	C02047_M	Enterobacter cloacae complex	s__Enterobacter cloacae	721	Caesarean	Mother	C
ERS2178530	C02059	C02059_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	168	Caesarean	Neonatal	C
ERS2178543	C02059	C02059_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	168	Caesarean	Neonatal	C
ERS2178544	C02059	C02059_7	Enterobacter cloacae complex	s__Enterobacter himalayensis	168	Caesarean	Neonatal	C
ERS2178880	A00908_T1	A00908_T1_21	Enterococcus casseliflavus	s__Enterococcus_D sp002850555		Caesarean	Neonatal	A
ERS2178720	A01057	A01057_21	Enterococcus casseliflavus	s__Enterococcus_D casseliflavus		Caesarean	Neonatal	A

ERS2443969	A01057	A01057_21	Enterococcus casseliflavus	s__Enterococcus_D casseliflavus		Caesarean	Neonatal	A
ERS2443970	A01057	A01057_4	Enterococcus casseliflavus	s__Enterococcus_D sp002850555		Caesarean	Neonatal	A
ERS2429202	B00092	B00092_21	Enterococcus casseliflavus	s__Enterococcus_D casseliflavus		Caesarean	Neonatal	B
ERS2429203	B00092	B00092_21	Enterococcus casseliflavus	s__Enterococcus_D casseliflavus		Caesarean	Neonatal	B
ERS2178930	B00537	B00537_M	Enterococcus casseliflavus	s__Enterococcus_D casseliflavus		Vaginal	Mother	B
ERS2178932	B00537	B00537_M	Enterococcus casseliflavus	s__Enterococcus_D casseliflavus		Vaginal	Mother	B
ERS2179014	C01329	C01329_7	Enterococcus casseliflavus	s__Enterococcus_D casseliflavus		Caesarean	Neonatal	C
ERS2295742	C01837	C01837_21	Enterococcus casseliflavus	s__Enterococcus_D casseliflavus		Caesarean	Neonatal	C
ERS2178752	A00190	A00190_21	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	A
ERS2178815	B00119	B00119_21	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178816	B00119	B00119_21	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178819	B00119	B00119_4	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178822	B00119	B00119_7	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178853	B00268	B00268_21	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178854	B00268	B00268_21	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178857	B00268	B00268_21	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178860	B00268	B00268_21	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178861	B00268	B00268_21	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178779	B01261	B01261_7	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178712	B01339	B01339_21	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	B
ERS2178976	B02005	B02005_M	Enterococcus durans	s__Enterococcus_B durans		Caesarean	Mother	B
ERS2295724	C01008_T2	C01008_T2_4	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Neonatal	C
ERS2179007	C01012	C01012_M	Enterococcus durans	s__Enterococcus_B durans		Caesarean	Mother	C
ERS2179037	C01752	C01752_M	Enterococcus durans	s__Enterococcus_B durans		Vaginal	Mother	C
ERS846588	512120	512120_9	Enterococcus faecalis	s__Enterococcus faecalis	19~	Caesarean	Neonatal	A
ERS2046351	514124	514124_7	Enterococcus faecalis	s__Enterococcus faecalis	97	Vaginal	Neonatal	A
ERS2046354	515126	515126_10	Enterococcus faecalis	s__Enterococcus faecalis	220	Vaginal	Neonatal	A
ERS846591	519128	519128_12	Enterococcus faecalis	s__Enterococcus faecalis	55	Caesarean	Neonatal	A
ERS2046345	521130	521130_10	Enterococcus faecalis	s__Enterococcus faecalis	191	Vaginal	Neonatal	A
ERS2295785	A00021_T1	A00021_T1_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295786	A00021_T1	A00021_T1_21	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	A
ERS2178745	A00021_T2	A00021_T2_7	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	A
ERS2295789	A00021_T2	A00021_T2_4	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295790	A00031	A00031_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2429160	A00043	A00043_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	A
ERS2295757	A00106	A00106_M	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Mother	A
ERS2429189	A00106_T1	A00106_T1_21	Enterococcus faecalis	s__Enterococcus faecalis	64	Vaginal	Neonatal	A
ERS2178646	A00106_T2	A00106_T2_21	Enterococcus faecalis	s__Enterococcus faecalis	64	Vaginal	Neonatal	A
ERS2429209	A00185	A00185_4	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	A
ERS2178749	A00190	A00190_21	Enterococcus faecalis	s__Enterococcus faecalis	30	Vaginal	Neonatal	A
ERS2178698	A00219	A00219_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2178594	A00502	A00502_21	Enterococcus faecalis	s__Enterococcus faecalis	40	Vaginal	Neonatal	A
ERS2429164	A00502	A00502_7	Enterococcus faecalis	s__Enterococcus faecalis	40	Vaginal	Neonatal	A
ERS2429210	A00502	A00502_4	Enterococcus faecalis	s__Enterococcus faecalis	40	Vaginal	Neonatal	A
ERS2178758	A00559	A00559_21	Enterococcus faecalis	s__Enterococcus faecalis	86~	Vaginal	Neonatal	A
ERS2178759	A00559	A00559_7	Enterococcus faecalis	s__Enterococcus faecalis	86~	Vaginal	Neonatal	A
ERS2178760	A00559	A00559_21	Enterococcus faecalis	s__Enterococcus faecalis	86~	Vaginal	Neonatal	A
ERS2178761	A00559	A00559_21	Enterococcus faecalis	s__Enterococcus faecalis	86~	Vaginal	Neonatal	A
ERS2178762	A00559	A00559_7	Enterococcus faecalis	s__Enterococcus faecalis	86~	Vaginal	Neonatal	A
ERS2179048	A00576	A00576_M	Enterococcus faecalis	s__Enterococcus faecalis	776	Vaginal	Mother	A
ERS2295799	A00576	A00576_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Neonatal	A
ERS2295805	A00576	A00576_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Mother	A
ERS2295806	A00576	A00576_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Mother	A
ERS2178665	A00908_T1	A00908_T1_4	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2178666	A00908_T1	A00908_T1_4	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2178667	A00908_T1	A00908_T1_4	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295810	A00908_T1	A00908_T1_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2444041	A00908_T1	A00908_T1_4	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2429165	A00947	A00947_4	Enterococcus faecalis	s__Enterococcus faecalis	4~	Caesarean	Neonatal	A
ERS2429181	A00947	A00947_21	Enterococcus faecalis	s__Enterococcus faecalis	4~	Caesarean	Neonatal	A
ERS2178763	A00995	A00995_7	Enterococcus faecalis	s__Enterococcus faecalis	30	Vaginal	Neonatal	A
ERS2178886	A00995	A00995_7	Enterococcus faecalis	s__Enterococcus faecalis	30	Vaginal	Neonatal	A
ERS2178887	A00995	A00995_7	Enterococcus faecalis	s__Enterococcus faecalis	30	Vaginal	Neonatal	A
ERS2295817	A00995	A00995_4	Enterococcus faecalis	s__Enterococcus faecalis	30	Vaginal	Neonatal	A
ERS2178764	A01011	A01011_4	Enterococcus faecalis	s__Enterococcus faecalis	8	Vaginal	Neonatal	A
ERS2178765	A01011	A01011_7	Enterococcus faecalis	s__Enterococcus faecalis	8	Vaginal	Neonatal	A
ERS2178718	A01057	A01057_21	Enterococcus faecalis	s__Enterococcus faecalis	72	Caesarean	Neonatal	A
ERS2178719	A01057	A01057_21	Enterococcus faecalis	s__Enterococcus faecalis	72	Caesarean	Neonatal	A
ERS2178888	A01057	A01057_4	Enterococcus faecalis	s__Enterococcus faecalis	72	Caesarean	Neonatal	A
ERS2178723	A01077	A01077_21	Enterococcus faecalis	s__Enterococcus faecalis	269	Caesarean	Neonatal	A
ERS2178724	A01077	A01077_21	Enterococcus faecalis	s__Enterococcus faecalis	269	Caesarean	Neonatal	A
ERS2178892	A01082	A01082_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2178893	A01082	A01082_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295797	A01082	A01082_4	Enterococcus faecalis	s__Enterococcus faecalis	257	Caesarean	Neonatal	A
ERS2295824	A01082	A01082_4	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2429190	A01082	A01082_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2178598	A01105	A01105_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295826	A01105	A01105_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295828	A01105	A01105_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2429166	A01105	A01105_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295829	A01107	A01107_4	Enterococcus faecalis	s__Enterococcus faecalis	25	Caesarean	Neonatal	A
ERS2295830	A01107	A01107_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Mother	A
ERS2295833	A01107	A01107_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Mother	A
ERS2295834	A01107	A01107_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Mother	A
ERS2178766	A01166	A01166_21	Enterococcus faecalis	s__Enterococcus faecalis	30~	Caesarean	Neonatal	A
ERS2178768	A01166	A01166_4	Enterococcus faecalis	s__Enterococcus faecalis	44~	Caesarean	Neonatal	A
ERS2178769	A01166	A01166_7	Enterococcus faecalis	s__Enterococcus faecalis	44~	Caesarean	Neonatal	A
ERS2178770	A01166	A01166_7	Enterococcus faecalis	s__Enterococcus faecalis	44~	Caesarean	Neonatal	A
ERS2429191	A01173	A01173_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2178599	A01176	A01176_4	Enterococcus faecalis	s__Enterococcus faecalis	308~	Caesarean	Neonatal	A
ERS2178894	A01176	A01176_7	Enterococcus faecalis	s__Enterococcus faecalis	308~	Caesarean	Neonatal	A
ERS2295835	A01176	A01176_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295836	A01176	A01176_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295837	A01176	A01176_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A

ERS2429167	A01176	A01176_4	Enterococcus faecalis	s__Enterococcus faecalis	308~	Caesarean	Neonatal	A
ERS2178771	A01301	A01301_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2178895	A01301	A01301_4	Enterococcus faecalis	s__Enterococcus faecalis	23	Caesarean	Neonatal	A
ERS2295838	A01301	A01301_7	Enterococcus faecalis	s__Enterococcus faecalis	23	Caesarean	Neonatal	A
ERS2178772	A01311	A01311_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2178773	A01311	A01311_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2178590	A01506	A01506_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2178774	A01563	A01563_7	Enterococcus faecalis	s__Enterococcus faecalis	241	Caesarean	Neonatal	A
ERS2178656	A01583	A01583_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295781	A01583	A01583_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2178668	A01586	A01586_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2178730	A01639	A01639_21	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	A
ERS2178732	A01639	A01639_7	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	A
ERS2178775	A01639	A01639_4	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	A
ERS2178776	A01639	A01639_4	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	A
ERS2295842	A01653	A01653_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2429161	A01671	A01671_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2429162	A01671	A01671_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2429163	A01671	A01671_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2178657	A01676	A01676_4	Enterococcus faecalis	s__Enterococcus faecalis	40	Caesarean	Neonatal	A
ERS2295843	A01676	A01676_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295844	A01676	A01676_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2429195	A01676	A01676_4	Enterococcus faecalis	s__Enterococcus faecalis	40	Caesarean	Neonatal	A
ERS2295845	A01678	A01678_21	Enterococcus faecalis	s__Enterococcus faecalis	44	Vaginal	Neonatal	A
ERS2429168	A01687	A01687_4	Enterococcus faecalis	s__Enterococcus faecalis	19	Caesarean	Neonatal	A
ERS2429169	A01687	A01687_7	Enterococcus faecalis	s__Enterococcus faecalis	19	Caesarean	Neonatal	A
ERS2429170	A01739	A01739_4	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	A
ERS2429171	A01739	A01739_7	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	A
ERS2178777	A01805	A01805_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	A
ERS2178650	A01862	A01862_4	Enterococcus faecalis	s__Enterococcus faecalis	168	Caesarean	Neonatal	A
ERS2295846	A01862	A01862_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295849	A01862	A01862_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295850	A01866	A01866_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295851	A01866	A01866_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295852	A01866	A01866_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295854	A01921	A01921_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	A
ERS2295856	A01921	A01921_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	A
ERS2295857	A01921	A01921_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	A
ERS2295858	A01921	A01921_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Neonatal	A
ERS2295860	A01939	A01939_4	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295862	A01939	A01939_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2178605	A01966	A01966_4	Enterococcus faecalis	s__Enterococcus faecalis	25	Caesarean	Neonatal	A
ERS2295863	A01966	A01966_7	Enterococcus faecalis	s__Enterococcus faecalis	25	Caesarean	Neonatal	A
ERS2429172	A01966	A01966_21	Enterococcus faecalis	s__Enterococcus faecalis	25	Caesarean	Neonatal	A
ERS2178675	A02053	A02053_21	Enterococcus faecalis	s__Enterococcus faecalis	40	Caesarean	Neonatal	A
ERS2295769	A02053	A02053_4	Enterococcus faecalis	s__Enterococcus faecalis	40	Caesarean	Neonatal	A
ERS2295770	A02053	A02053_7	Enterococcus faecalis	s__Enterococcus faecalis	40	Caesarean	Neonatal	A
ERS2295771	A02053	A02053_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2178631	A02110	A02110_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295864	A02110	A02110_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295865	A02110	A02110_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295866	A02110	A02110_M	Enterococcus faecalis	s__Enterococcus faecalis	23	Caesarean	Mother	A
ERS2295867	A02110	A02110_M	Enterococcus faecalis	s__Enterococcus faecalis	23	Caesarean	Mother	A
ERS2429182	A02110	A02110_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2429183	A02110	A02110_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2429211	A02110	A02110_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	A
ERS2295870	A02138	A02138_21	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2295873	A02819	A02819_7	Enterococcus faecalis	s__Enterococcus faecalis	23	Caesarean	Neonatal	A
ERS2295874	A02913	A02913_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Neonatal	A
ERS2443988	B00010	B00010_4	Enterococcus faecalis	s__Enterococcus faecalis	133	Caesarean	Neonatal	B
ERS2178634	B00012	B00012_7	Enterococcus faecalis	s__Enterococcus faecalis	16~	Vaginal	Neonatal	B
ERS2178635	B00012	B00012_7	Enterococcus faecalis	s__Enterococcus faecalis	16~	Vaginal	Neonatal	B
ERS2295748	B00012	B00012_M	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Mother	B
ERS2429173	B00012	B00012_4	Enterococcus faecalis	s__Enterococcus faecalis	16~	Vaginal	Neonatal	B
ERS2178784	B00013	B00013_4	Enterococcus faecalis	s__Enterococcus faecalis	191	Vaginal	Neonatal	B
ERS2178785	B00013	B00013_7	Enterococcus faecalis	s__Enterococcus faecalis	191	Vaginal	Neonatal	B
ERS2178786	B00013	B00013_7	Enterococcus faecalis	s__Enterococcus faecalis	191	Vaginal	Neonatal	B
ERS2295752	B00013	B00013_21	Enterococcus faecalis	s__Enterococcus faecalis	191	Vaginal	Neonatal	B
ERS2295877	B00016	B00016_21	Enterococcus faecalis	s__Enterococcus faecalis	56	Caesarean	Neonatal	B
ERS2178787	B00020	B00020_4	Enterococcus faecalis	s__Enterococcus faecalis	295	Vaginal	Neonatal	B
ERS2178790	B00020	B00020_7	Enterococcus faecalis	s__Enterococcus faecalis	295	Vaginal	Neonatal	B
ERS2178904	B00020	B00020_21	Enterococcus faecalis	s__Enterococcus faecalis	295	Vaginal	Neonatal	B
ERS2429174	B00036	B00036_4	Enterococcus faecalis	s__Enterococcus faecalis	30~	Vaginal	Neonatal	B
ERS2429175	B00036	B00036_21	Enterococcus faecalis	s__Enterococcus faecalis	30~	Vaginal	Neonatal	B
ERS2429192	B00036	B00036_7	Enterococcus faecalis	s__Enterococcus faecalis	30~	Vaginal	Neonatal	B
ERS2295875	B00046	B00046_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Mother	B
ERS2178611	B00053	B00053_4	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	B
ERS2178907	B00053	B00053_7	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	B
ERS2178793	B00071	B00071_7	Enterococcus faecalis	s__Enterococcus faecalis	41	Caesarean	Neonatal	B
ERS2178794	B00071	B00071_21	Enterococcus faecalis	s__Enterococcus faecalis	41	Caesarean	Neonatal	B
ERS2178795	B00085	B00085_7	Enterococcus faecalis	s__Enterococcus faecalis	135	Caesarean	Neonatal	B
ERS2178702	B00088	B00088_7	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	B
ERS2295878	B00090	B00090_4	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Neonatal	B
ERS2295763	B00092	B00092_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2295764	B00092	B00092_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2178788	B00097	B00097_21	Enterococcus faecalis	s__Enterococcus faecalis	22	Vaginal	Neonatal	B
ERS2178804	B00097	B00097_21	Enterococcus faecalis	s__Enterococcus faecalis	22	Vaginal	Neonatal	B
ERS2178612	B00100	B00100_7	Enterococcus faecalis	s__Enterococcus faecalis	40	Vaginal	Neonatal	B
ERS2429177	B00100	B00100_21	Enterococcus faecalis	s__Enterococcus faecalis	40	Vaginal	Neonatal	B
ERS2178614	B00101	B00101_4	Enterococcus faecalis	s__Enterococcus faecalis	34	Vaginal	Neonatal	B
ERS2178615	B00101	B00101_7	Enterococcus faecalis	s__Enterococcus faecalis	34	Vaginal	Neonatal	B
ERS2178652	B00101	B00101_21	Enterococcus faecalis	s__Enterococcus faecalis	34	Vaginal	Neonatal	B
ERS2178908	B00111	B00111_4	Enterococcus faecalis	s__Enterococcus faecalis	5~	Caesarean	Neonatal	B
ERS2178909	B00111	B00111_7	Enterococcus faecalis	s__Enterococcus faecalis	5~	Caesarean	Neonatal	B

ERS2178705	B00116	B00116_7	Enterococcus faecalis	s__Enterococcus faecalis	283	Caesarean	Neonatal	B
ERS2178706	B00116	B00116_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2429204	B00116	B00116_4	Enterococcus faecalis	s__Enterococcus faecalis	283	Caesarean	Neonatal	B
ERS2178823	B00120	B00120_7	Enterococcus faecalis	s__Enterococcus faecalis	205	Caesarean	Neonatal	B
ERS2178636	B00129	B00129_7	Enterococcus faecalis	s__Enterococcus faecalis	81	Caesarean	Neonatal	B
ERS2178616	B00157_T3	B00157_T3_4	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	B
ERS2178827	B00178	B00178_21	Enterococcus faecalis	s__Enterococcus faecalis	40	Caesarean	Neonatal	B
ERS2178829	B00178	B00178_21	Enterococcus faecalis	s__Enterococcus faecalis	268	Caesarean	Neonatal	B
ERS2178830	B00178	B00178_7	Enterococcus faecalis	s__Enterococcus faecalis	268	Caesarean	Neonatal	B
ERS2178707	B00203_T1	B00203_T1_21	Enterococcus faecalis	s__Enterococcus faecalis	102	Caesarean	Neonatal	B
ERS2178832	B00203_T1	B00203_T1_7	Enterococcus faecalis	s__Enterococcus faecalis	102	Caesarean	Neonatal	B
ERS2178833	B00203_T1	B00203_T1_7	Enterococcus faecalis	s__Enterococcus faecalis	102	Caesarean	Neonatal	B
ERS2178831	B00203_T2	B00203_T2_21	Enterococcus faecalis	s__Enterococcus faecalis	102	Caesarean	Neonatal	B
ERS2178834	B00203_T2	B00203_T2_7	Enterococcus faecalis	s__Enterococcus faecalis	102	Caesarean	Neonatal	B
ERS2178835	B00203_T2	B00203_T2_7	Enterococcus faecalis	s__Enterococcus faecalis	102	Caesarean	Neonatal	B
ERS2178836	B00203_T2	B00203_T2_7	Enterococcus faecalis	s__Enterococcus faecalis	102	Caesarean	Neonatal	B
ERS2429178	B00203_T2	B00203_T2_4	Enterococcus faecalis	s__Enterococcus faecalis	102	Caesarean	Neonatal	B
ERS2443996	B00203_T2	B00203_T2_21	Enterococcus faecalis	s__Enterococcus faecalis	102	Caesarean	Neonatal	B
ERS2178837	B00235	B00235_7	Enterococcus faecalis	s__Enterococcus faecalis	26	Vaginal	Neonatal	B
ERS2295879	B00235	B00235_21	Enterococcus faecalis	s__Enterococcus faecalis	26	Vaginal	Neonatal	B
ERS2178838	B00236	B00236_21	Enterococcus faecalis	s__Enterococcus faecalis	28	Vaginal	Neonatal	B
ERS2178842	B00236	B00236_7	Enterococcus faecalis	s__Enterococcus faecalis	28	Vaginal	Neonatal	B
ERS2178843	B00236	B00236_4	Enterococcus faecalis	s__Enterococcus faecalis	28	Vaginal	Neonatal	B
ERS2178844	B00236	B00236_4	Enterococcus faecalis	s__Enterococcus faecalis	28	Vaginal	Neonatal	B
ERS2178618	B00272	B00272_4	Enterococcus faecalis	s__Enterococcus faecalis	535	Caesarean	Neonatal	B
ERS2178863	B00272	B00272_21	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	B
ERS2429184	B00272	B00272_7	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	B
ERS2429185	B00272	B00272_7	Enterococcus faecalis	s__Enterococcus faecalis	535	Caesarean	Neonatal	B
ERS2178922	B00507	B00507_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2178864	B00518	B00518_4	Enterococcus faecalis	s__Enterococcus faecalis	40~	Caesarean	Neonatal	B
ERS2178865	B00518	B00518_4	Enterococcus faecalis	s__Enterococcus faecalis	40~	Caesarean	Neonatal	B
ERS2178866	B00518	B00518_7	Enterococcus faecalis	s__Enterococcus faecalis	40~	Caesarean	Neonatal	B
ERS2178927	B00518	B00518_21	Enterococcus faecalis	s__Enterococcus faecalis	40~	Caesarean	Neonatal	B
ERS2429186	B00518	B00518_7	Enterococcus faecalis	s__Enterococcus faecalis	40~	Caesarean	Neonatal	B
ERS2178934	B00550	B00550_21	Enterococcus faecalis	s__Enterococcus faecalis	44	Caesarean	Neonatal	B
ERS2178867	B00553	B00553_21	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	B
ERS2178868	B00553	B00553_21	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	B
ERS2444001	B00553	B00553_7	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	B
ERS2429198	B00922	B00922_7	Enterococcus faecalis	s__Enterococcus faecalis	23	Vaginal	Neonatal	B
ERS2178936	B01021	B01021_21	Enterococcus faecalis	s__Enterococcus faecalis	603~	Caesarean	Neonatal	B
ERS2429205	B01042	B01042_M	Enterococcus faecalis	s__Enterococcus faecalis	59	Caesarean	Mother	B
ERS2429206	B01042	B01042_M	Enterococcus faecalis	s__Enterococcus faecalis	19	Caesarean	Mother	B
ERS2429207	B01042	B01042_M	Enterococcus faecalis	s__Enterococcus faecalis	19	Caesarean	Mother	B
ERS2178664	B01089	B01089_7	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	B
ERS2178938	B01196	B01196_21	Enterococcus faecalis	s__Enterococcus faecalis	34	Vaginal	Neonatal	B
ERS2178942	B01236	B01236_7	Enterococcus faecalis	s__Enterococcus faecalis	669~	Caesarean	Neonatal	B
ERS2178943	B01236	B01236_21	Enterococcus faecalis	s__Enterococcus faecalis	669~	Caesarean	Neonatal	B
ERS2178778	B01261	B01261_7	Enterococcus faecalis	s__Enterococcus faecalis	44	Vaginal	Neonatal	B
ERS2178944	B01261	B01261_21	Enterococcus faecalis	s__Enterococcus faecalis	44	Vaginal	Neonatal	B
ERS2295694	B01278	B01278_7	Enterococcus faecalis	s__Enterococcus faecalis	145	Caesarean	Neonatal	B
ERS2295695	B01278	B01278_21	Enterococcus faecalis	s__Enterococcus faecalis	145	Caesarean	Neonatal	B
ERS2443999	B01278	B01278_4	Enterococcus faecalis	s__Enterococcus faecalis	145	Caesarean	Neonatal	B
ERS2178711	B01339	B01339_21	Enterococcus faecalis	s__Enterococcus faecalis	21	Vaginal	Neonatal	B
ERS2178713	B01339	B01339_7	Enterococcus faecalis	s__Enterococcus faecalis	21	Vaginal	Neonatal	B
ERS2178949	B01339	B01339_4	Enterococcus faecalis	s__Enterococcus faecalis	21	Vaginal	Neonatal	B
ERS2429187	B01365	B01365_21	Enterococcus faecalis	s__Enterococcus faecalis	25	Caesarean	Neonatal	B
ERS2178953	B01375	B01375_4	Enterococcus faecalis	s__Enterococcus faecalis	19	Vaginal	Neonatal	B
ERS2178954	B01375	B01375_7	Enterococcus faecalis	s__Enterococcus faecalis	19	Vaginal	Neonatal	B
ERS2178955	B01471	B01471_M	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Mother	B
ERS2178956	B01471	B01471_M	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Mother	B
ERS2295697	B01610	B01610_21	Enterococcus faecalis	s__Enterococcus faecalis	81	Vaginal	Neonatal	B
ERS2443987	B01610	B01610_7	Enterococcus faecalis	s__Enterococcus faecalis	81	Vaginal	Neonatal	B
ERS2178964	B01719	B01719_21	Enterococcus faecalis	s__Enterococcus faecalis	40	Vaginal	Neonatal	B
ERS2178965	B01719	B01719_4	Enterococcus faecalis	s__Enterococcus faecalis	40	Vaginal	Neonatal	B
ERS2178966	B01719	B01719_7	Enterococcus faecalis	s__Enterococcus faecalis	40	Vaginal	Neonatal	B
ERS2178653	B01772	B01772_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2295701	B01772	B01772_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2429196	B01772	B01772_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2429197	B01772	B01772_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2178715	B01775	B01775_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	B
ERS2295706	B01775	B01775_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	B
ERS2295708	B01775	B01775_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	B
ERS2178969	B01797	B01797_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	B
ERS2178970	B01797	B01797_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	B
ERS2178971	B01956	B01956_4	Enterococcus faecalis	s__Enterococcus faecalis	21	Vaginal	Neonatal	B
ERS2178973	B02005	B02005_21	Enterococcus faecalis	s__Enterococcus faecalis	308~	Caesarean	Neonatal	B
ERS2178975	B02005	B02005_7	Enterococcus faecalis	s__Enterococcus faecalis	64~	Caesarean	Neonatal	B
ERS2178980	B02156	B02156_21	Enterococcus faecalis	s__Enterococcus faecalis	40~	Vaginal	Neonatal	B
ERS2178981	B02156	B02156_21	Enterococcus faecalis	s__Enterococcus faecalis	40~	Vaginal	Neonatal	B
ERS2295712	B02211	B02211_21	Enterococcus faecalis	s__Enterococcus faecalis	30	Vaginal	Neonatal	B
ERS2295713	B02211	B02211_7	Enterococcus faecalis	s__Enterococcus faecalis	30	Vaginal	Neonatal	B
ERS2178669	B02215	B02215_21	Enterococcus faecalis	s__Enterococcus faecalis	197	Caesarean	Neonatal	B
ERS2429200	B02215	B02215_21	Enterococcus faecalis	s__Enterococcus faecalis	197	Caesarean	Neonatal	B
ERS2429201	B02215	B02215_21	Enterococcus faecalis	s__Enterococcus faecalis	197	Caesarean	Neonatal	B
ERS2178717	B02216	B02216_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2295717	B02216	B02216_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2178982	B02257	B02257_21	Enterococcus faecalis	s__Enterococcus faecalis	191	Vaginal	Neonatal	B
ERS2295721	B02258	B02258_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	B
ERS2295722	B02258	B02258_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	B
ERS2178988	B02270	B02270_4	Enterococcus faecalis	s__Enterococcus faecalis	28	Caesarean	Neonatal	B
ERS2178989	B02270	B02270_7	Enterococcus faecalis	s__Enterococcus faecalis	28	Caesarean	Neonatal	B
ERS2178990	B02273	B02273_4	Enterococcus faecalis	s__Enterococcus faecalis	209	Vaginal	Neonatal	B
ERS2178991	B02273	B02273_7	Enterococcus faecalis	s__Enterococcus faecalis	517	Vaginal	Neonatal	B
ERS2178992	B02315	B02315_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B

ERS2178993	B02315	B02315_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2178996	B02326	B02326_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	B
ERS2178997	B02588	B02588_4	Enterococcus faecalis	s__Enterococcus faecalis	41	Vaginal	Neonatal	B
ERS2295723	B02588	B02588_7	Enterococcus faecalis	s__Enterococcus faecalis	41	Vaginal	Neonatal	B
ERS2178998	B02720	B02720_4	Enterococcus faecalis	s__Enterococcus faecalis	415	Vaginal	Neonatal	B
ERS2179000	B02720	B02720_7	Enterococcus faecalis	s__Enterococcus faecalis	415	Vaginal	Neonatal	B
ERS2179001	B02720	B02720_21	Enterococcus faecalis	s__Enterococcus faecalis	415	Vaginal	Neonatal	B
ERS2046479	S6	S6_7	Enterococcus faecalis	s__Enterococcus faecalis	372	Vaginal	Neonatal	A
ERS2295725	C01008_T2	C01008_T2_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	C
ERS2179005	C01012	C01012_21	Enterococcus faecalis	s__Enterococcus faecalis	21~	Caesarean	Neonatal	C
ERS2179006	C01012	C01012_21	Enterococcus faecalis	s__Enterococcus faecalis	21~	Caesarean	Neonatal	C
ERS2179008	C01052	C01052_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	C
ERS2295728	C01052	C01052_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	C
ERS2295729	C01052	C01052_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	C
ERS2179011	C01075	C01075_M	Enterococcus faecalis	s__Enterococcus faecalis	290	Vaginal	Mother	C
ERS2295730	C01201	C01201_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	C
ERS2295731	C01201	C01201_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	C
ERS2179013	C01329	C01329_4	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	C
ERS2179015	C01329	C01329_7	Enterococcus faecalis	s__Enterococcus faecalis	191	Caesarean	Neonatal	C
ERS2179017	C01331	C01331_4	Enterococcus faecalis	s__Enterococcus faecalis	133	Caesarean	Neonatal	C
ERS2179018	C01387	C01387_4	Enterococcus faecalis	s__Enterococcus faecalis	64	Vaginal	Neonatal	C
ERS2429188	C01387	C01387_7	Enterococcus faecalis	s__Enterococcus faecalis	64	Vaginal	Neonatal	C
ERS2429208	C01387	C01387_M	Enterococcus faecalis	s__Enterococcus faecalis	22	Vaginal	Mother	C
ERS2295732	C01389	C01389_7	Enterococcus faecalis	s__Enterococcus faecalis	472	Caesarean	Neonatal	C
ERS2295733	C01389	C01389_21	Enterococcus faecalis	s__Enterococcus faecalis	472	Caesarean	Neonatal	C
ERS2295735	C01389	C01389_4	Enterococcus faecalis	s__Enterococcus faecalis	472	Caesarean	Neonatal	C
ERS2179023	C01392	C01392_21	Enterococcus faecalis	s__Enterococcus faecalis	23	Caesarean	Neonatal	C
ERS2179024	C01392	C01392_21	Enterococcus faecalis	s__Enterococcus faecalis	23	Caesarean	Neonatal	C
ERS2179025	C01392	C01392_21	Enterococcus faecalis	s__Enterococcus faecalis	23	Caesarean	Neonatal	C
ERS2179026	C01443	C01443_M	Enterococcus faecalis	s__Enterococcus faecalis	19	Caesarean	Mother	C
ERS2295736	C01529	C01529_7	Enterococcus faecalis	s__Enterococcus faecalis	40	Caesarean	Neonatal	C
ERS2429179	C01529	C01529_4	Enterococcus faecalis	s__Enterococcus faecalis	40	Caesarean	Neonatal	C
ERS2178620	C01530	C01530_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2178642	C01530	C01530_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2178643	C01530	C01530_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2178644	C01530	C01530_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2295737	C01530	C01530_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2179029	C01560	C01560_7	Enterococcus faecalis	s__Enterococcus faecalis	133	Vaginal	Neonatal	C
ERS2178621	C01695	C01695_4	Enterococcus faecalis	s__Enterococcus faecalis	878	Caesarean	Neonatal	C
ERS2178622	C01695	C01695_4	Enterococcus faecalis	s__Enterococcus faecalis	206~	Caesarean	Neonatal	C
ERS2178737	C01700	C01700_7	Enterococcus faecalis	s__Enterococcus faecalis	117	Caesarean	Neonatal	C
ERS2179030	C01700	C01700_7	Enterococcus faecalis	s__Enterococcus faecalis	117	Caesarean	Neonatal	C
ERS2179031	C01700	C01700_4	Enterococcus faecalis	s__Enterococcus faecalis	117	Caesarean	Neonatal	C
ERS2295738	C01700	C01700_4	Enterococcus faecalis	s__Enterococcus faecalis	179~	Caesarean	Neonatal	C
ERS2178623	C01751	C01751_4	Enterococcus faecalis	s__Enterococcus faecalis	878	Caesarean	Neonatal	C
ERS2179033	C01752	C01752_4	Enterococcus faecalis	s__Enterococcus faecalis	64	Vaginal	Neonatal	C
ERS2179042	C01757	C01757_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2178625	C01758	C01758_7	Enterococcus faecalis	s__Enterococcus faecalis	776	Vaginal	Neonatal	C
ERS2179043	C01758	C01758_21	Enterococcus faecalis	s__Enterococcus faecalis	776	Vaginal	Neonatal	C
ERS2179045	C01758	C01758_21	Enterococcus faecalis	s__Enterococcus faecalis	97	Vaginal	Neonatal	C
ERS2295804	C01758	C01758_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Mother	C
ERS2429180	C01758	C01758_4	Enterococcus faecalis	s__Enterococcus faecalis	776	Vaginal	Neonatal	C
ERS2179049	C01832	C01832_4	Enterococcus faecalis	s__Enterococcus faecalis	179~	Vaginal	Neonatal	C
ERS2295739	C01832	C01832_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	C
ERS2295740	C01832	C01832_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Vaginal	Neonatal	C
ERS2179050	C01837	C01837_4	Enterococcus faecalis	s__Enterococcus faecalis	26	Caesarean	Neonatal	C
ERS2295741	C01837	C01837_21	Enterococcus faecalis	s__Enterococcus faecalis	26	Caesarean	Neonatal	C
ERS2179051	C01839	C01839_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Neonatal	C
ERS2179053	C01841	C01841_M	Enterococcus faecalis	s__Enterococcus faecalis	49~	Vaginal	Mother	C
ERS2179055	C01871	C01871_M	Enterococcus faecalis	s__Enterococcus faecalis	84	Vaginal	Mother	C
ERS2179056	C01877	C01877_21	Enterococcus faecalis	s__Enterococcus faecalis	97	Caesarean	Neonatal	C
ERS2179057	C01877	C01877_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2429193	C01913	C01913_7	Enterococcus faecalis	s__Enterococcus faecalis	30	Caesarean	Neonatal	C
ERS2178626	C01919	C01919_4	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2178627	C01919	C01919_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2178628	C01919	C01919_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2429118	C01919	C01919_21	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2429128	C01929	C01929_7	Enterococcus faecalis	s__Enterococcus faecalis	44	Vaginal	Neonatal	C
ERS2178629	C01930	C01930_4	Enterococcus faecalis	s__Enterococcus faecalis	669~	Caesarean	Neonatal	C
ERS2295745	C01930	C01930_7	Enterococcus faecalis	s__Enterococcus faecalis	669~	Caesarean	Neonatal	C
ERS2295746	C01930	C01930_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2295747	C01930	C01930_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2429129	C01930	C01930_21	Enterococcus faecalis	s__Enterococcus faecalis	669~	Caesarean	Neonatal	C
ERS2429130	C01930	C01930_21	Enterococcus faecalis	s__Enterococcus faecalis	669~	Caesarean	Neonatal	C
ERS2429138	C02047	C02047_M	Enterococcus faecalis	s__Enterococcus faecalis	369	Caesarean	Mother	C
ERS2429139	C02047	C02047_M	Enterococcus faecalis	s__Enterococcus faecalis	369	Caesarean	Mother	C
ERS2429194	C02059	C02059_7	Enterococcus faecalis	s__Enterococcus faecalis	40	Caesarean	Neonatal	C
ERS2429146	C02062	C02062_21	Enterococcus faecalis	s__Enterococcus faecalis	23	Vaginal	Neonatal	C
ERS2429148	C02180	C02180_7	Enterococcus faecalis	s__Enterococcus faecalis	81	Vaginal	Neonatal	C
ERS2429149	C02180	C02180_7	Enterococcus faecalis	s__Enterococcus faecalis	81	Vaginal	Neonatal	C
ERS2178872	C02186	C02186_7	Enterococcus faecalis	s__Enterococcus faecalis	19	Vaginal	Neonatal	C
ERS2178873	C02186	C02186_7	Enterococcus faecalis	s__Enterococcus faecalis	19	Vaginal	Neonatal	C
ERS2429153	C02223_T2	C02223_T2_7	Enterococcus faecalis	s__Enterococcus faecalis	55	Caesarean	Neonatal	C
ERS2178740	C02236	C02236_7	Enterococcus faecalis	s__Enterococcus faecalis	55	Caesarean	Neonatal	C
ERS2295787	C02295	C02295_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Mother	C
ERS2295788	C02295	C02295_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Caesarean	Mother	C
ERS2295793	C02391	C02391_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Neonatal	C
ERS2295807	C02391	C02391_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Neonatal	C
ERS2295808	C02391	C02391_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Neonatal	C
ERS2295816	C02391	C02391_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Neonatal	C
ERS2178741	C02566	C02566_7	Enterococcus faecalis	s__Enterococcus faecalis	145	Caesarean	Neonatal	C
ERS2178742	C02566	C02566_7	Enterococcus faecalis	s__Enterococcus faecalis	145	Caesarean	Neonatal	C
ERS2178743	C02566	C02566_7	Enterococcus faecalis	s__Enterococcus faecalis	145	Caesarean	Neonatal	C
ERS2178744	C02566	C02566_M	Enterococcus faecalis	s__Enterococcus faecalis	55	Caesarean	Mother	C

ERS2295823	C02695	C02695_M	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Mother	C
ERS2178994	C02756	C02756_M	Enterococcus faecalis	s__Enterococcus faecalis	21	Caesarean	Mother	C
ERS2295841	C02756	C02756_7	Enterococcus faecalis	s__Enterococcus faecalis	179	Caesarean	Neonatal	C
ERS2295876	C02892	C02892_7	Enterococcus faecalis	s__Enterococcus faecalis	16	Vaginal	Neonatal	C
ERS2178876	A00021_T1	A00021_T1_21	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	A
ERS2178746	A00021_T2	A00021_T2_7	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	A
ERS2178750	A00190	A00190_21	Enterococcus faecium	s__Enterococcus_B faecium		Vaginal	Neonatal	A
ERS2178751	A00190	A00190_21	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Neonatal	A
ERS2178699	A00219	A00219_21	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	A
ERS2178755	A00219	A00219_7	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	A
ERS2178878	A00219	A00219_4	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	A
ERS2295809	A00908_T1	A00908_T1_21	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	A
ERS2178889	A01057	A01057_4	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	A
ERS2295818	A01057	A01057_4	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	A
ERS2443977	A01580	A01580_21	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	A
ERS2443981	A01580	A01580_21	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	A
ERS2178899	A01802	A01802_7	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	A
ERS2178900	A01802	A01802_7	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	A
ERS2178901	A01802	A01802_4	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	A
ERS2443986	A01802	A01802_4	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	A
ERS2295859	A01939	A01939_4	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	A
ERS2429176	B00036	B00036_4	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Neonatal	B
ERS2295751	B00046	B00046_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	B
ERS2178805	B00097	B00097_21	Enterococcus faecium	s__Enterococcus_B faecium		Vaginal	Neonatal	B
ERS2178811	B00097	B00097_7	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Neonatal	B
ERS2178826	B00178	B00178_21	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	B
ERS2178828	B00178	B00178_21	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	B
ERS2178845	B00252	B00252_4	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	B
ERS2178846	B00252	B00252_4	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	B
ERS2178847	B00252	B00252_21	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	B
ERS2178848	B00252	B00252_7	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	B
ERS2178849	B00252	B00252_7	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	B
ERS2178928	B00537	B00537_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	B
ERS2178929	B00537	B00537_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	B
ERS2178931	B00537	B00537_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	B
ERS2429199	B00922	B00922_7	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Neonatal	B
ERS2178676	B01042	B01042_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Mother	B
ERS2178677	B01042	B01042_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Mother	B
ERS2444000	B01278	B01278_21	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	B
ERS3418481	B01278	B01278_21	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	B
ERS2178958	B01616	B01616_4	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Neonatal	B
ERS2178959	B01616	B01616_7	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Neonatal	B
ERS2295699	B01616	B01616_21	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Neonatal	B
ERS2178961	B01716	B01716_M	Enterococcus faecium	s__Enterococcus_B faecium		Vaginal	Mother	B
ERS2178962	B01716	B01716_M	Enterococcus faecium	s__Enterococcus_B faecium		Vaginal	Mother	B
ERS2178963	B01716	B01716_M	Enterococcus faecium	s__Enterococcus_B faecium		Vaginal	Mother	B
ERS2178659	B01772	B01772_7	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	B
ERS2443990	B01772	B01772_21	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	B
ERS2178972	B02005	B02005_21	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Neonatal	B
ERS2178974	B02005	B02005_7	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	B
ERS2178986	B02263	B02263_M	Enterococcus faecium	s__Enterococcus_B faecium		Vaginal	Mother	B
ERS2178987	B02263	B02263_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	B
ERS2179009	C01075	C01075_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	C
ERS2179010	C01075	C01075_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	C
ERS2179012	C01201	C01201_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	C
ERS2179020	C01389	C01389_M	Enterococcus faecium	s__Enterococcus_A avium		Caesarean	Mother	C
ERS2179052	C01841	C01841_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	C
ERS2179054	C01844	C01844_M	Enterococcus faecium	s__Enterococcus_B faecium		Vaginal	Mother	C
ERS2429117	C01919	C01919_21	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Neonatal	C
ERS2429131	C01930	C01930_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Caesarean	Mother	C
ERS2295819	C02695	C02695_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	C
ERS2295822	C02695	C02695_M	Enterococcus faecium	s__Enterococcus_B faecium_B		Vaginal	Mother	C
ERS2295839	C02695	C02695_M	Enterococcus faecium	s__Enterococcus_B faecium		Vaginal	Mother	C
ERS2178977	C02756	C02756_M	Enterococcus faecium	s__Enterococcus_B faecium		Caesarean	Mother	C
ERS2295840	C02892	C02892_7	Enterococcus faecium	s__Enterococcus_B faecium		Vaginal	Neonatal	C
ERS2178789	B00097	B00097_21	Enterococcus gallinarum	s__Enterococcus_D gallinarum		Vaginal	Neonatal	B
ERS2178810	B00097	B00097_7	Enterococcus gallinarum	s__Enterococcus_D gallinarum		Vaginal	Neonatal	B
ERS2178855	B00268	B00268_21	Enterococcus gallinarum	s__Enterococcus_D sp002850555		Vaginal	Neonatal	B
ERS2178856	B00268	B00268_21	Enterococcus gallinarum	s__Enterococcus_D sp002850555		Vaginal	Neonatal	B
ERS2178714	B01775	B01775_21	Enterococcus gallinarum	s__Enterococcus_D sp002850555		Vaginal	Neonatal	B
ERS2178716	B01775	B01775_21	Enterococcus gallinarum	s__Enterococcus_D sp002850555		Vaginal	Neonatal	B
ERS2179004	C01010	C01010_M	Enterococcus gallinarum	s__Enterococcus_D gallinarum		Caesarean	Mother	C
ERS2179027	C01488	C01488_M	Enterococcus mundtii	s__Enterococcus_B mundtii		Caesarean	Mother	C
ERS2046344	521130	521130_10	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	A
ERS2178874	A00021_T1	A00021_T1_21	Escherichia coli	s__Escherichia coli		Caesarean	Neonatal	A
ERS2178747	A00021_T2	A00021_T2_7	Escherichia coli	s__Escherichia coli		Caesarean	Neonatal	A
ERS2178748	A00021_T2	A00021_T2_21	Escherichia coli	s__Escherichia coli		Caesarean	Neonatal	A
ERS2178877	A00067	A00067_21	Escherichia coli	s__Escherichia coli_D		Vaginal	Neonatal	A
ERS2178551	A00106_T2	A00106_T2_21	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	A
ERS2444036	A00106_T2	A00106_T2_21	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	A
ERS2295803	A00576	A00576_21	Escherichia coli	s__Escherichia flexneri		Vaginal	Neonatal	A
ERS2295812	A00908	A00908_M	Escherichia coli	s__Escherichia flexneri		Caesarean	Mother	A
ERS2295815	A00908	A00908_M	Escherichia coli	s__Escherichia flexneri		Caesarean	Mother	A
ERS2178890	A01082	A01082_21	Escherichia coli	s__Escherichia coli_D		Caesarean	Neonatal	A
ERS2178734	A01639	A01639_7	Escherichia coli	s__Escherichia coli		Caesarean	Neonatal	A
ERS2178903	B00016	B00016_21	Escherichia coli	s__Escherichia coli_D		Caesarean	Neonatal	B
ERS2295750	B00046	B00046_M	Escherichia coli	s__Escherichia coli		Vaginal	Mother	B
ERS2178821	B00119	B00119_4	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	B
ERS2178916	B00176	B00176_21	Escherichia coli	s__Escherichia coli_D		Vaginal	Neonatal	B
ERS2444002	B00553	B00553_7	Escherichia coli	s__Escherichia flexneri		Caesarean	Neonatal	B
ERS2178945	B01261	B01261_21	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	B
ERS2295696	B01278	B01278_21	Escherichia coli	s__Escherichia coli		Caesarean	Neonatal	B
ERS2178967	B01772	B01772_M	Escherichia coli	s__Escherichia coli		Caesarean	Mother	B
ERS2178968	B01772	B01772_M	Escherichia coli	s__Escherichia coli		Caesarean	Mother	B

ERS2295715	B02215	B02215_7	Escherichia coli	s__Escherichia coli_D		Caesarean	Neonatal	B
ERS2295716	B02215	B02215_4	Escherichia coli	s__Escherichia coli_D		Caesarean	Neonatal	B
ERS2178983	B02257	B02257_21	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	B
ERS2178985	B02257	B02257_21	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	B
ERS2878990	S19	S19_7	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	A
ERS2046478	S6	S6_7	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	A
ERS2295727	C01008_T2	C01008_T2_4	Escherichia coli	s__Escherichia coli_D		Vaginal	Neonatal	C
ERS2179021	C01389	C01389_21	Escherichia coli	s__Escherichia flexneri		Caesarean	Neonatal	C
ERS2179034	C01752	C01752_M	Escherichia coli	s__Escherichia flexneri		Vaginal	Mother	C
ERS2295743	C01837	C01837_21	Escherichia coli	s__Escherichia coli_D		Caesarean	Neonatal	C
ERS2429141	C02047	C02047_M	Escherichia coli	s__Escherichia coli_D		Caesarean	Mother	C
ERS2429145	C02062	C02062_21	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	C
ERS2295811	C02391	C02391_7	Escherichia coli	s__Escherichia coli		Vaginal	Neonatal	C
ERS2429156	C02565	C02565_M	Escherichia coli	s__Escherichia flexneri		Caesarean	Mother	C
ERS2444020	C02565	C02565_7	Escherichia coli	s__Escherichia coli		Caesarean	Neonatal	C
ERS2429157	C02571	C02571_M	Escherichia coli	s__Escherichia coli_D		Vaginal	Mother	C
ERS2429158	C02571	C02571_M	Escherichia coli	s__Escherichia coli_D		Vaginal	Mother	C
ERS2429159	C02571	C02571_M	Escherichia coli	s__Escherichia coli_D		Vaginal	Mother	C
ERS2178710	B00268	B00268_7	Escherichia hermannii	s__Atlantibacter hermannii		Vaginal	Neonatal	B
ERS2178906	B00053	B00053_7	Escherichia vulneris	s__Pseudescherichia vulneris		Caesarean	Neonatal	B
ERS2295798	A00576	A00576_21	Klebsiella aerogenes	s__Klebsiella_B aerogenes	141	Vaginal	Neonatal	A
ERS2178561	A00908_T1	A00908_T1_4	Klebsiella aerogenes	s__Klebsiella_B aerogenes	135	Caesarean	Neonatal	A
ERS2295831	A01107	A01107_M	Klebsiella aerogenes	s__Klebsiella_B aerogenes	148~	Caesarean	Mother	A
ERS2295832	A01107	A01107_M	Klebsiella aerogenes	s__Klebsiella_B aerogenes	148~	Caesarean	Mother	A
ERS2178978	B02118	B02118_7	Klebsiella aerogenes	s__Klebsiella_B aerogenes	188	Vaginal	Neonatal	B
ERS2178979	B02118	B02118_7	Klebsiella aerogenes	s__Klebsiella_B aerogenes	188	Vaginal	Neonatal	B
ERS2178738	C02236	C02236_7	Klebsiella aerogenes	s__Klebsiella_B aerogenes	110	Caesarean	Neonatal	C
ERS2295758	A00106	A00106_M	Klebsiella oxytoca	s__Klebsiella_A michiganensis	107~	Vaginal	Mother	A
ERS2295777	A00185	A00185_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	202	Caesarean	Neonatal	A
ERS2178756	A00219	A00219_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	50	Caesarean	Neonatal	A
ERS2178757	A00219	A00219_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	50	Caesarean	Neonatal	A
ERS2295801	A00576	A00576_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	29	Vaginal	Neonatal	A
ERS2178879	A00908_T1	A00908_T1_4	Klebsiella oxytoca	s__Klebsiella_A oxytoca	20~	Caesarean	Neonatal	A
ERS2178881	A00908_T1	A00908_T1_21	Klebsiella oxytoca	s__Klebsiella_A oxytoca	20~	Caesarean	Neonatal	A
ERS2178721	A01057	A01057_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	261~	Caesarean	Neonatal	A
ERS2178722	A01057	A01057_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	214~	Caesarean	Neonatal	A
ERS2178725	A01077	A01077_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	29	Caesarean	Neonatal	A
ERS2178726	A01077	A01077_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	29	Caesarean	Neonatal	A
ERS2178727	A01077	A01077_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	29	Caesarean	Neonatal	A
ERS2178552	A01082	A01082_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	214~	Caesarean	Neonatal	A
ERS2178555	A01082	A01082_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	214~	Caesarean	Neonatal	A
ERS2178896	A01301	A01301_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	71~	Caesarean	Neonatal	A
ERS2178897	A01301	A01301_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	71~	Caesarean	Neonatal	A
ERS2178898	A01301	A01301_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	71~	Caesarean	Neonatal	A
ERS2178728	A01580	A01580_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	88	Caesarean	Neonatal	A
ERS2178729	A01580	A01580_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	88	Caesarean	Neonatal	A
ERS2295782	A01583	A01583_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Caesarean	Neonatal	A
ERS2295783	A01583	A01583_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Caesarean	Neonatal	A
ERS2178581	A01586	A01586_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	29	Caesarean	Neonatal	A
ERS2178731	A01639	A01639_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	44~	Caesarean	Neonatal	A
ERS2178733	A01639	A01639_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	44~	Caesarean	Neonatal	A
ERS2178559	A01676	A01676_4	Klebsiella oxytoca	s__Klebsiella_A oxytoca	36	Caesarean	Neonatal	A
ERS2178536	A01862	A01862_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	216~	Caesarean	Neonatal	A
ERS2295847	A01862	A01862_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	216~	Caesarean	Neonatal	A
ERS2295848	A01862	A01862_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	216~	Caesarean	Neonatal	A
ERS2444040	A01862	A01862_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	216~	Caesarean	Neonatal	A
ERS2295861	A01939	A01939_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	97~	Caesarean	Neonatal	A
ERS2178513	A02110	A02110_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	157	Caesarean	Neonatal	A
ERS2178514	A02110	A02110_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	157	Caesarean	Neonatal	A
ERS2178515	A02110	A02110_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	157	Caesarean	Neonatal	A
ERS2295869	A02138	A02138_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	227	Caesarean	Neonatal	A
ERS2295779	B00027	B00027_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	177	Vaginal	Neonatal	B
ERS2178582	B00036	B00036_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	216	Vaginal	Neonatal	B
ERS2444015	B00036	B00036_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	108	Vaginal	Neonatal	B
ERS2178497	B00053	B00053_21	Klebsiella oxytoca	s__Klebsiella_A oxytoca	199	Caesarean	Neonatal	B
ERS2178700	B00088	B00088_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	91~	Caesarean	Neonatal	B
ERS2295759	B00092	B00092_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	40	Caesarean	Neonatal	B
ERS2295761	B00092	B00092_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	40	Caesarean	Neonatal	B
ERS2295762	B00092	B00092_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	40	Caesarean	Neonatal	B
ERS2178796	B00096	B00096_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	184	Caesarean	Neonatal	B
ERS2178798	B00096	B00096_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	76~	Caesarean	Neonatal	B
ERS2178799	B00096	B00096_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	76~	Caesarean	Neonatal	B
ERS2178800	B00096	B00096_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	76~	Caesarean	Neonatal	B
ERS2178801	B00096	B00096_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	76~	Caesarean	Neonatal	B
ERS2178803	B00096	B00096_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	184	Caesarean	Neonatal	B
ERS2178685	B00097	B00097_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	184~	Vaginal	Neonatal	B
ERS2178686	B00097	B00097_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	91~	Vaginal	Neonatal	B
ERS2178703	B00097	B00097_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	184	Vaginal	Neonatal	B
ERS2178806	B00097	B00097_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	173~	Vaginal	Neonatal	B
ERS2178807	B00097	B00097_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	173~	Vaginal	Neonatal	B
ERS2178808	B00097	B00097_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	173~	Vaginal	Neonatal	B
ERS2178809	B00097	B00097_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	173~	Vaginal	Neonatal	B
ERS2178812	B00097	B00097_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	173	Vaginal	Neonatal	B
ERS2178813	B00097	B00097_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	173~	Vaginal	Neonatal	B
ERS2178814	B00097	B00097_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	173~	Vaginal	Neonatal	B
ERS2178687	B00116	B00116_7	Klebsiella oxytoca	s__Klebsiella_A oxytoca	37	Caesarean	Neonatal	B
ERS2178688	B00116	B00116_7	Klebsiella oxytoca	s__Klebsiella_A oxytoca	37	Caesarean	Neonatal	B
ERS2295765	B00116	B00116_4	Klebsiella oxytoca	s__Klebsiella_A oxytoca	37	Caesarean	Neonatal	B
ERS2178817	B00119	B00119_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	168	Vaginal	Neonatal	B
ERS2178910	B00136	B00136_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Caesarean	Neonatal	B
ERS2178911	B00136	B00136_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Caesarean	Neonatal	B
ERS2178912	B00136	B00136_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Caesarean	Neonatal	B
ERS2178913	B00136	B00136_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Caesarean	Neonatal	B
ERS2178914	B00136	B00136_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Caesarean	Neonatal	B

ERS2178915	B00136	B00136_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Caesarean	Neonatal	B
ERS2295767	B00139	B00139_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	40	Caesarean	Neonatal	B
ERS2295768	B00139	B00139_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	215~	Caesarean	Neonatal	B
ERS2178565	B00174	B00174_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	108	Caesarean	Neonatal	B
ERS2178566	B00174	B00174_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	88	Caesarean	Neonatal	B
ERS2178567	B00174	B00174_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	88	Caesarean	Neonatal	B
ERS2178570	B00174	B00174_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	215	Caesarean	Neonatal	B
ERS2178571	B00174	B00174_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	108	Caesarean	Neonatal	B
ERS2178572	B00174	B00174_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	88	Caesarean	Neonatal	B
ERS2178573	B00174	B00174_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	88	Caesarean	Neonatal	B
ERS2178825	B00178	B00178_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	186	Caesarean	Neonatal	B
ERS2178691	B00203_T1	B00203_T1_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	186	Caesarean	Neonatal	B
ERS2178840	B00236	B00236_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	184~	Vaginal	Neonatal	B
ERS2178841	B00236	B00236_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	184~	Vaginal	Neonatal	B
ERS2178850	B00252	B00252_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	91~	Caesarean	Neonatal	B
ERS2178708	B00268	B00268_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	216	Vaginal	Neonatal	B
ERS2178709	B00268	B00268_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	109	Vaginal	Neonatal	B
ERS2178852	B00268	B00268_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	134~	Vaginal	Neonatal	B
ERS2178859	B00268	B00268_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	109	Vaginal	Neonatal	B
ERS2178862	B00268	B00268_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	246~	Vaginal	Neonatal	B
ERS2178516	B00562_T2	B00562_T2_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	44	Caesarean	Neonatal	B
ERS2178575	B00562_T2	B00562_T2_4	Klebsiella oxytoca	s__Klebsiella_A oxytoca	37	Caesarean	Neonatal	B
ERS2178869	B00917	B00917_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	216	Vaginal	Neonatal	B
ERS2178870	B00917	B00917_21	Klebsiella oxytoca	s__Klebsiella_A oxytoca	20	Vaginal	Neonatal	B
ERS2178871	B00917	B00917_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	216	Vaginal	Neonatal	B
ERS2178577	B00922	B00922_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	168	Vaginal	Neonatal	B
ERS2178937	B01021	B01021_21	Klebsiella oxytoca	s__Klebsiella_A oxytoca	58	Caesarean	Neonatal	B
ERS2178498	B01089	B01089_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	85	Caesarean	Neonatal	B
ERS2178499	B01089	B01089_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	85	Caesarean	Neonatal	B
ERS2178500	B01089	B01089_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	263	Caesarean	Neonatal	B
ERS2178579	B01089	B01089_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	263	Caesarean	Neonatal	B
ERS2444026	B01089	B01089_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	263	Caesarean	Neonatal	B
ERS2178947	B01261	B01261_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	186	Vaginal	Neonatal	B
ERS2178957	B01572	B01572_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	225	Vaginal	Neonatal	B
ERS2178587	B01616	B01616_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	71~	Vaginal	Neonatal	B
ERS2178524	B01772	B01772_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	11~	Caesarean	Neonatal	B
ERS2178525	B01772	B01772_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	234~	Caesarean	Neonatal	B
ERS2178526	B01772	B01772_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	234~	Caesarean	Neonatal	B
ERS2178527	B01772	B01772_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	234~	Caesarean	Neonatal	B
ERS2178540	B01772	B01772_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	11~	Caesarean	Neonatal	B
ERS2178541	B01772	B01772_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	11~	Caesarean	Neonatal	B
ERS2178542	B01772	B01772_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	11~	Caesarean	Neonatal	B
ERS2178693	B01775	B01775_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Vaginal	Neonatal	B
ERS2178694	B01775	B01775_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	40	Vaginal	Neonatal	B
ERS2295702	B01775	B01775_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	246	Vaginal	Neonatal	B
ERS2295703	B01775	B01775_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Vaginal	Neonatal	B
ERS2295704	B01775	B01775_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	246	Vaginal	Neonatal	B
ERS2295705	B01775	B01775_4	Klebsiella oxytoca	s__Klebsiella_A grimontii	246	Vaginal	Neonatal	B
ERS2295710	B01775	B01775_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Vaginal	Neonatal	B
ERS2295711	B01775	B01775_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Vaginal	Neonatal	B
ERS2178588	B02215	B02215_4	Klebsiella oxytoca	s__Klebsiella_A oxytoca	258	Caesarean	Neonatal	B
ERS2295714	B02215	B02215_7	Klebsiella oxytoca	s__Klebsiella_A oxytoca	258	Caesarean	Neonatal	B
ERS2178999	B02720	B02720_4	Klebsiella oxytoca	s__Klebsiella_A oxytoca	36	Vaginal	Neonatal	B
ERS2179002	B02722	B02722_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	85	Caesarean	Neonatal	B
ERS2179003	B02722	B02722_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	85	Caesarean	Neonatal	B
ERS2046477	S2	S2_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	216	Caesarean	Neonatal	A
ERS2295726	C01008_T2	C01008_T2_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	44	Vaginal	Neonatal	C
ERS2295734	C01389	C01389_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	50	Caesarean	Neonatal	C
ERS2295773	C01757	C01757_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	50	Caesarean	Neonatal	C
ERS2295774	C01757	C01757_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	168	Caesarean	Neonatal	C
ERS2295775	C01757	C01757_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	71~	Caesarean	Neonatal	C
ERS2295776	C01757	C01757_4	Klebsiella oxytoca	s__Klebsiella_A michiganensis	202~	Caesarean	Neonatal	C
ERS2179044	C01758	C01758_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	13	Vaginal	Neonatal	C
ERS2179047	C01758	C01758_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	40~	Vaginal	Neonatal	C
ERS2179036	C01877	C01877_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	186	Caesarean	Neonatal	C
ERS2179058	C01877	C01877_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	186	Caesarean	Neonatal	C
ERS2179059	C01877	C01877_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	126~	Caesarean	Neonatal	C
ERS2179060	C01877	C01877_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	85	Caesarean	Neonatal	C
ERS2429119	C01919	C01919_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	151	Caesarean	Neonatal	C
ERS2429120	C01919	C01919_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	151	Caesarean	Neonatal	C
ERS2429121	C01919	C01919_21	Klebsiella oxytoca	s__Klebsiella_A michiganensis	151	Caesarean	Neonatal	C
ERS2429124	C01919	C01919_M	Klebsiella oxytoca	s__Klebsiella_A michiganensis	213	Caesarean	Mother	C
ERS2429125	C01919	C01919_M	Klebsiella oxytoca	s__Klebsiella_A grimontii	184~	Caesarean	Mother	C
ERS2429133	C02016	C02016_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	185	Caesarean	Neonatal	C
ERS2429134	C02016	C02016_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	185~	Caesarean	Neonatal	C
ERS2429135	C02016	C02016_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	185~	Caesarean	Neonatal	C
ERS2429136	C02016	C02016_21	Klebsiella oxytoca	s__Klebsiella_A grimontii	185~	Caesarean	Neonatal	C
ERS2429142	C02047	C02047_M	Klebsiella oxytoca	s__Klebsiella_A oxytoca	30~	Caesarean	Mother	C
ERS2429147	C02062	C02062_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	29	Vaginal	Neonatal	C
ERS2429150	C02180	C02180_7	Klebsiella oxytoca	s__Klebsiella_A michiganensis	177	Vaginal	Neonatal	C
ERS2178739	C02236	C02236_7	Klebsiella oxytoca	s__Klebsiella_A oxytoca	22~	Caesarean	Neonatal	C
ERS2429155	C02391	C02391_7	Klebsiella oxytoca	s__Klebsiella_A oxytoca	22~	Vaginal	Neonatal	C
ERS2295853	C02892	C02892_7	Klebsiella oxytoca	s__Klebsiella_A grimontii	172~	Vaginal	Neonatal	C
ERS2178875	A00021_T1	A00021_T1_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	70	Caesarean	Neonatal	A
ERS2295791	A00031	A00031_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2452	Caesarean	Neonatal	A
ERS2295792	A00031	A00031_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2452	Caesarean	Neonatal	A
ERS2178494	A00043	A00043_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2452	Vaginal	Neonatal	A
ERS2178495	A00043	A00043_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2452	Vaginal	Neonatal	A
ERS2178496	A00043	A00043_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2452	Vaginal	Neonatal	A
ERS2178532	A00106_T1	A00106_T1_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	559~	Vaginal	Neonatal	A
ERS2295794	A00576	A00576_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	4387	Vaginal	Neonatal	A
ERS2295802	A00576	A00576_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	4387	Vaginal	Neonatal	A
ERS2295813	A00908	A00908_M	Klebsiella pneumoniae	s__Klebsiella variicola	360~	Caesarean	Mother	A
ERS2295814	A00908	A00908_M	Klebsiella pneumoniae	s__Klebsiella pneumoniae	643~	Caesarean	Mother	A

ERS2178517	A01082	A01082_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	559~	Caesarean	Neonatal	A
ERS2178518	A01082	A01082_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	559~	Caesarean	Neonatal	A
ERS2178553	A01082	A01082_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	559~	Caesarean	Neonatal	A
ERS2178554	A01082	A01082_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	559~	Caesarean	Neonatal	A
ERS2295795	A01082	A01082_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	559~	Caesarean	Neonatal	A
ERS2295796	A01082	A01082_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	559~	Caesarean	Neonatal	A
ERS2295821	A01082	A01082_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	35	Caesarean	Neonatal	A
ERS2295827	A01105	A01105_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	35	Caesarean	Neonatal	A
ERS2178519	A01173	A01173_7	Klebsiella pneumoniae	s__Klebsiella variicola	3353	Caesarean	Neonatal	A
ERS2295778	A01173	A01173_21	Klebsiella pneumoniae	s__Klebsiella variicola	3353	Caesarean	Neonatal	A
ERS2444030	A01173	A01173_7	Klebsiella pneumoniae	s__Klebsiella variicola	3353	Caesarean	Neonatal	A
ERS2295753	A01671	A01671_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	1079	Caesarean	Neonatal	A
ERS2295784	A01671	A01671_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	1079	Caesarean	Neonatal	A
ERS2178902	A01866	A01866_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	827~	Caesarean	Neonatal	A
ERS2295868	A02133	A02133_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2805	Vaginal	Neonatal	A
ERS2295871	A02138	A02138_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	188	Caesarean	Neonatal	A
ERS2295872	A02138	A02138_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	188	Caesarean	Neonatal	A
ERS2295749	B00046	B00046_M	Klebsiella pneumoniae	s__Klebsiella pneumoniae	105	Vaginal	Mother	B
ERS2178824	B00120	B00120_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	323	Caesarean	Neonatal	B
ERS2178689	B00203_T1	B00203_T1_21	Klebsiella pneumoniae	s__Klebsiella quasipneumoniae	4216~	Caesarean	Neonatal	B
ERS2178690	B00203_T1	B00203_T1_21	Klebsiella pneumoniae	s__Klebsiella quasipneumoniae	4216~	Caesarean	Neonatal	B
ERS2178692	B00203_T1	B00203_T1_21	Klebsiella pneumoniae	s__Klebsiella quasipneumoniae	4216~	Caesarean	Neonatal	B
ERS2178923	B00507	B00507_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	188	Caesarean	Neonatal	B
ERS2178924	B00507	B00507_4	Klebsiella pneumoniae	s__Klebsiella pneumoniae	359	Caesarean	Neonatal	B
ERS2178925	B00507	B00507_4	Klebsiella pneumoniae	s__Klebsiella pneumoniae	188	Caesarean	Neonatal	B
ERS2178926	B00507	B00507_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	359	Caesarean	Neonatal	B
ERS2178935	B00550	B00550_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	922	Caesarean	Neonatal	B
ERS2178939	B01196	B01196_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	922	Vaginal	Neonatal	B
ERS2178940	B01196	B01196_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	20	Vaginal	Neonatal	B
ERS2178941	B01196	B01196_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	922	Vaginal	Neonatal	B
ERS2178946	B01261	B01261_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	469	Vaginal	Neonatal	B
ERS2178948	B01261	B01261_21	Klebsiella pneumoniae	s__Klebsiella quasipneumoniae	1676	Vaginal	Neonatal	B
ERS2178960	B01712	B01712_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	461	Caesarean	Neonatal	B
ERS2295707	B01775	B01775_4	Klebsiella pneumoniae	s__Klebsiella pneumoniae	1877	Vaginal	Neonatal	B
ERS2295709	B01775	B01775_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	1877	Vaginal	Neonatal	B
ERS2178697	B02216	B02216_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	1877	Caesarean	Neonatal	B
ERS2295719	B02216	B02216_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	1877	Caesarean	Neonatal	B
ERS2295720	B02216	B02216_4	Klebsiella pneumoniae	s__Klebsiella pneumoniae	1877	Caesarean	Neonatal	B
ERS2178984	B02257	B02257_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	1412	Vaginal	Neonatal	B
ERS2178505	C01689	C01689_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	268	Caesarean	Neonatal	C
ERS2178507	C01689	C01689_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	268	Caesarean	Neonatal	C
ERS2178508	C01689	C01689_4	Klebsiella pneumoniae	s__Klebsiella pneumoniae	268	Caesarean	Neonatal	C
ERS2178509	C01689	C01689_4	Klebsiella pneumoniae	s__Klebsiella pneumoniae	268	Caesarean	Neonatal	C
ERS2178510	C01689	C01689_4	Klebsiella pneumoniae	s__Klebsiella pneumoniae	268	Caesarean	Neonatal	C
ERS2178511	C01689	C01689_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	268	Caesarean	Neonatal	C
ERS2444028	C01689	C01689_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	268	Caesarean	Neonatal	C
ERS2444029	C01689	C01689_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	268	Caesarean	Neonatal	C
ERS2295754	C01752	C01752_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	1877	Vaginal	Neonatal	C
ERS2179046	C01758	C01758_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	422	Vaginal	Neonatal	C
ERS2295744	C01837	C01837_21	Klebsiella pneumoniae	s__Klebsiella variicola	2594~	Caesarean	Neonatal	C
ERS2295756	C01913	C01913_21	Klebsiella pneumoniae	s__Klebsiella variicola	639	Caesarean	Neonatal	C
ERS2444034	C01913	C01913_7	Klebsiella pneumoniae	s__Klebsiella variicola	639	Caesarean	Neonatal	C
ERS2179061	C01917	C01917_M	Klebsiella pneumoniae	s__Klebsiella pneumoniae	111	Vaginal	Mother	C
ERS2179062	C01917	C01917_M	Klebsiella pneumoniae	s__Klebsiella pneumoniae	111	Vaginal	Mother	C
ERS2429122	C01919	C01919_M	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2990	Caesarean	Mother	C
ERS2429123	C01919	C01919_M	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2990	Caesarean	Mother	C
ERS2429126	C01919	C01919_M	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2990	Caesarean	Mother	C
ERS2429127	C01919	C01919_M	Klebsiella pneumoniae	s__Klebsiella pneumoniae	2990	Caesarean	Mother	C
ERS2429137	C02047	C02047_M	Klebsiella pneumoniae	s__Klebsiella pneumoniae	45	Caesarean	Mother	C
ERS2429140	C02047	C02047_M	Klebsiella pneumoniae	s__Klebsiella quasipneumoniae	1901	Caesarean	Mother	C
ERS2429144	C02047	C02047_M	Klebsiella pneumoniae	s__Klebsiella quasipneumoniae	1901	Caesarean	Mother	C
ERS2178695	C02097	C02097_21	Klebsiella pneumoniae	s__Klebsiella pneumoniae	104~	Vaginal	Neonatal	C
ERS2178696	C02097	C02097_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	104~	Vaginal	Neonatal	C
ERS2295691	C02186	C02186_7	Klebsiella pneumoniae	s__Klebsiella variicola	4146	Vaginal	Neonatal	C
ERS2429151	C02223_T1	C02223_T1_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	661	Caesarean	Neonatal	C
ERS2429152	C02223_T2	C02223_T2_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	661	Caesarean	Neonatal	C
ERS2429154	C02223_T2	C02223_T2_7	Klebsiella pneumoniae	s__Klebsiella pneumoniae	661	Caesarean	Neonatal	C
ERS846590	512120	512120_9	Lactobacillus gasseri	s__Lactobacillus gasseri_A		Caesarean	Neonatal	A
ERS2046355	515126	515126_10	Lactobacillus paracasei	s__Lactobacillus_C paracasei		Vaginal	Neonatal	A
ERS2046343	513122	513122_4	Lactobacillus rhamnosus	s__Lactobacillus_C rhamnosus		Vaginal	Neonatal	A
ERS2444010	B02255	B02255_21	Lactobacillus rhamnosus	s__Lactobacillus_C rhamnosus		Caesarean	Neonatal	B
ERS2178783	B00002	B00002_7	Lelliottia amnigena	s__Lelliottia lapagei		Caesarean	Neonatal	B
ERS3418479	B00507	B00507_21	Raoultella ornithinolytica	s__Raoultella ornithinolytica		Caesarean	Neonatal	B
ERS3418480	C01990	C01990_21	Raoultella ornithinolytica	s__Raoultella ornithinolytica		Vaginal	Neonatal	C
ERS3418477	B00097	B00097_21	Raoultella planticola	s__Raoultella planticola		Vaginal	Neonatal	B
ERS2443974	A01176	A01176_21	Serratia marcescens	s__Serratia marcescens_B		Caesarean	Neonatal	A
ERS2444023	B02326	B02326_21	Serratia marcescens	s__Serratia marcescens_I		Caesarean	Neonatal	B
ERS2444022	B02118	B02118_7	Staphylococcus aureus	s__Staphylococcus aureus		Vaginal	Neonatal	B
ERS2444024	B00097	B00097_4	Staphylococcus epidermidis	s__Staphylococcus epidermidis		Vaginal	Neonatal	B
ERS2178933	B00550	B00550_21	Staphylococcus epidermidis	s__Staphylococcus epidermidis		Caesarean	Neonatal	B
ERS2178995	B02326	B02326_4	Staphylococcus epidermidis	s__Staphylococcus epidermidis		Caesarean	Neonatal	B
ERS2179019	C01389	C01389_M	Staphylococcus epidermidis	s__Staphylococcus epidermidis		Caesarean	Mother	C
ERS2179032	C01700	C01700_7	Staphylococcus epidermidis	s__Staphylococcus epidermidis		Caesarean	Neonatal	C
ERS2046340	S19	S19_7	Streptococcus lutetiensis	s__Streptococcus lutetiensis		Vaginal	Neonatal	A
ERS2178950	B01339	B01339_4	Streptococcus mitis	g__Streptococcus		Vaginal	Neonatal	B

Appendix 6 Accessions and metadata of the WGS public isolates

Accessions and metadata of the public genomes included in WGS analysis.

Accession	Species	Source	Reference
GCA_000499025	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000390685	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000390725	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000647995	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648015	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648035	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648055	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648075	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648095	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648115	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648135	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648155	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648175	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000648195	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000788155	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000788165	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000788175	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000788185	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000788235	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_000788255	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_001598635	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_001766735	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_001878755	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_001878765	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_001878785	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_001931845	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
GCF_001932015	Enterococcus faecalis	Environmental	GTDBv86; PMID: 30148503
ERS2046320	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046333	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS846581	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS846587	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS846588	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS846591	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046513	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046514	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046515	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046541	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046546	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046391	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046412	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046424	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046430	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
ERS2046436	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
GCA_003438055	Enterococcus faecalis	Healthy Human Gut Microbiota	CGR; PMID: 30718868
GCF_000147295	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
GCF_000147455	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
GCF_000147475	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
GCF_000147495	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
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GCF_000690925	Enterococcus faecalis	Healthy Human Gut Microbiota	HGG; PMID: 30718869
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ERS325530	Enterococcus faecalis	UK Hospitals	PMID: 27572164
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ERS325844	Enterococcus faecalis	UK Hospitals	PMID: 27572164
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ERS325741	Enterococcus faecalis	UK Hospitals	PMID: 27572164
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ERS339172	Enterococcus faecalis	UK Hospitals	PMID: 27572164
GCA_000264705	Enterobacter cloacae complex	Environmental	GTDBv86; PMID: 30148503
GCA_000286655	Enterobacter cloacae complex	Environmental	GTDBv86; PMID: 30148503
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ERS381195	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381196	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381197	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381198	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381199	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381200	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381201	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381202	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381203	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381204	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381205	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381206	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381207	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381208	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381209	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381210	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381211	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381213	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381214	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381215	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381216	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381217	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381218	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381228	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381242	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381243	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381244	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459

ERS381245	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381246	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381247	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381248	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381249	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381251	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381263	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381265	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381266	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381268	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381269	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381270	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381272	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381273	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381274	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381275	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381277	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381279	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381280	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381281	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS380921	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS380924	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS380930	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS380938	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS380959	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS380972	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS380981	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS380988	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS380989	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381016	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381021	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381028	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381035	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381047	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381049	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381057	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381063	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381075	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381087	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381088	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381090	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381091	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381103	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381105	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381111	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381115	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381117	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381118	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381124	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381125	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381127	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381129	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381133	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381134	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381140	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
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ERS381146	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381158	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381168	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381169	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381175	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381177	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381183	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381184	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459
ERS381267	Klebsiella pneumoniae	UK Hospitals	PMID: 28223459

Appendix 7 Accessions of the 100 public gut metagenomes

A list of accession numbers of 100 public gut metagenomes used in the Kraken classification benchmarking.

ERR011136
ERR011182
ERR011195
ERR011202
ERR011251
ERR1018243
ERR1293553
ERR1293620
ERR1293664
ERR1293669
ERR1293687
ERR1293704
ERR1293773
ERR1293890
ERR2013639
ERR209079
ERR209085
ERR209116
ERR209158
ERR209162
ERR209178
ERR209228
ERR209231
ERR209252
ERR209332
ERR209370
ERR209380
ERR209442
ERR209464
ERR209643
ERR209653
ERR209674
ERR209703
ERR209832
ERR321076
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ERR321345
ERR321355
ERR321407
ERR321453
ERR321458
ERR321479
ERR321504
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ERR321561
ERR321565
ERR321566
ERR321593
ERR321616
ERR321648
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ERR414253
ERR414262
ERR414386
ERR414394
ERR414399
ERR414497
ERR414500
ERR414502
ERR636351
ERR636358
ERR636359
ERR636368
ERR636383
ERR636408
ERR912053
ERR912178
SRR1761705
SRR1761711
SRR1930253
SRR2726244
SRR2992890
SRR2992892
SRR2992896
SRR2992919
SRR2992920
SRR2992931
SRR2992932
SRR2992958
SRR2992967
SRR3917619
SRR3992999
SRR5127592
SRR5127613
SRR5127654
SRR5127661
SRR5127728
SRR5127733
SRR5127765
SRR5127782
SRR5127842

Appendix 8 Eukaryotic metagenome-assembled genome bins

A list of 356 genome bins predicted to belong to eukaryotic organisms.

Sample ID	Subject ID	Source	Delivery mode	Bin ID	Bin length	% Bin aligned	Reference ID	Reference length	Reference	Mash distance	ANI (%)	Reference organism	Kingdom
20596_4_12	B00012	Neonatal	Vaginal	20596_4_12_bin.1	13651928	99.62	GCA_000775455.1_Cand_albi_L26_V	14516741	94.82	0.00	99.45	Candida albicans	Fungi
18403_21	BBS0006	Neonatal	Vaginal	18403_21_bin.13	13698717	99.26	GCA_000773725.1_Cand_albi_P7804	14503432	94.44	0.00	99.48	Candida albicans	Fungi
21940_3_10	B01712	Neonatal	Caesarean	21940_3_10_bin.2	13632292	99.59	GCA_000447475.1_Cand_albi_A92_V	14607426	94.38	0.00	99.48	Candida albicans	Fungi
21127_7_17	B01089	Neonatal	Caesarean	21127_7_17_bin.4	13573992	99.13	GCA_000774085.1_Cand_albi_P87_V	14461023	94.38	0.00	99.4	Candida albicans	Fungi
20596_5_18	B00046	Neonatal	Vaginal	20596_5_18_bin.17	13795153	98.86	GCA_000784495.1_Cand_albi_P7606	14622326	94.2	0.00	99.33	Candida albicans	Fungi
21842_3_8	B01616	Neonatal	Vaginal	21842_3_8_bin.1	13570714	99.38	GCA_000447575.1_Cand_albi_A20_V	14553017	94.04	0.00	99.56	Candida albicans	Fungi
19646_5_8	BBS0038	Neonatal	Vaginal	19646_5_8_bin.13	13650167	99.14	GCA_000447635.1_Cand_albi_A84_V	14691637	93.91	0.00	99.52	Candida albicans	Fungi
20596_5_11	B00040	Neonatal	Vaginal	20596_5_11_bin.6	13522012	99.48	GCA_003454735.1_ASM345473v1	14425299	93.75	0.00	99.02	Candida albicans	Fungi
21673_46	B01234	Neonatal	Vaginal	21673_46_bin.2	13528462	99.4	GCA_000775445.1_Cand_albi_19F_V	14573765	93.52	0.00	99.59	Candida albicans	Fungi
24211_6_10	B02287	Neonatal	Vaginal	24211_6_10_bin.2	13359532	99.25	GCA_000447615.1_Cand_albi_A155_	14465145	93.25	0.01	99.18	Candida albicans	Fungi
21673_12	A01301	Neonatal	Caesarean	21673_12_bin.6	13856861	98.14	GCA_005890765.1_ASM589076v1	14699975	92.99	0.01	98.82	Candida albicans	Fungi
20727_7_1	B00096	Neonatal	Caesarean	20727_7_1_bin.8	13586748	99.6	GCA_000447495.1_Cand_albi_A203_	14785429	92.93	0.00	99.32	Candida albicans	Fungi
22178_5_8	B02106	Neonatal	Caesarean	22178_5_8_bin.1	13374250	98.26	GCA_000784495.1_Cand_albi_P7606	14622326	91	0.00	99.04	Candida albicans	Fungi
23584_4_19	C02756	Neonatal	Caesarean	23584_4_19_bin.7	13215399	98.53	GCA_000773735.1_Cand_albi_GC75_	14696915	90.45	0.02	99.12	Candida albicans	Fungi
19646_4_18	S37_T1	Neonatal	Vaginal	19646_4_18_bin.1	13187633	99	GCA_000784575.1_Cand_albi_P7501	14862837	88.69	0.00	99.46	Candida albicans	Fungi
22607_2_7	B01829	Neonatal	Vaginal	22607_2_7_bin.6	12298829	98.03	GCA_000784595.1_Cand_albi_P7501	14680338	83.31	0.01	98.79	Candida albicans	Fungi
25076_7_11	B02779	Infancy	Caesarean	25076_7_11_bin.24	8768381	92.28	GCA_002276455.1_ASM227645v1	17071403	57.57	0.02	98.35	Candida albicans	Fungi
22607_2_8	B01829	Neonatal	Vaginal	22607_2_8_bin.3	7990978	96.83	GCA_000773735.1_Cand_albi_GC75_	14696915	54.28	0.02	98.17	Candida albicans	Fungi
24211_6_18	C02406	Neonatal	Vaginal	24211_6_18_bin.6	5386964	91.68	GCA_004026255.1_ASM402625v1	12561678	39.77	0.03	98.5	Candida albicans	Fungi
23164_7_19	B02720	Neonatal	Vaginal	23164_7_19_bin.4	5230494	98.95	GCA_000773805.1_Cand_albi_P5707	14509911	36.64	0.03	98.48	Candida albicans	Fungi
25013_3_6	B01242	Neonatal	Caesarean	25013_3_6_bin.1	5486108	85.45	GCA_002259875.1_ASM225987v1	15640028	32.09	0.03	98.15	Candida albicans	Fungi
21842_4_7	C01529	Neonatal	Caesarean	21842_4_7_bin.10	5800027	73.43	GCA_002259805.1_ASM225980v1	15264541	29.84	0.04	97.77	Candida albicans	Fungi
20596_4_11	B00012	Neonatal	Vaginal	20596_4_11_bin.7	2868281	97.39	GCA_000447595.1_Cand_albi_3153A	14889980	19.79	0.05	97.74	Candida albicans	Fungi
20596_5_7	B00036	Neonatal	Vaginal	20596_5_7_bin.7	2192308	86.13	GCA_000773805.1_Cand_albi_P5707	14509911	13.58	0.07	97.12	Candida albicans	Fungi
22607_2_12	B01829	Neonatal	Vaginal	22607_2_12_bin.12	1357562	96.02	GCA_000784695.1_Cand_albi_Ca6_V	14716334	9.53	0.09	97.85	Candida albicans	Fungi
23164_6_11	C01837	Neonatal	Caesarean	23164_6_11_bin.1	1147277	97.44	GCA_000447635.1_Cand_albi_A84_V	14691637	8.23	0.10	98.26	Candida albicans	Fungi
22607_3_20	B02326	Neonatal	Caesarean	22607_3_20_bin.5	314052	95.45	GCA_005890765.1_ASM589076v1	14699975	2.26	0.13	97.36	Candida albicans	Fungi
20727_7_2	B00096	Neonatal	Caesarean	20727_7_2_bin.14	251238	95.4	GCA_000149445.2_ASM14944v2	14472953	1.82	0.19	97.33	Candida albicans	Fungi
22607_3_20	B02326	Neonatal	Caesarean	22607_3_20_bin.8	223617	95.24	GCA_000773735.1_Cand_albi_GC75_	14696915	1.49	0.16	97.63	Candida albicans	Fungi
22178_5_5	B02098	Neonatal	Caesarean	22178_5_5_bin.1	12493329	99.24	GCA_000982555.2_CBS6318.1	13050515	94.6	0.00	99.91	Candida parapsilosis	Fungi
21242_4	A01166	Neonatal	Caesarean	21242_4_bin.5	11281297	97.88	GCA_004026445.1_ASM402644v1	12563647	88.54	0.01	99.06	Candida parapsilosis	Fungi
19646_5_23	BBS0062	Neonatal	Caesarean	19646_5_23_bin.3	10707109	97.91	GCA_004026445.1_ASM402644v1	12563647	84.16	0.01	98.89	Candida parapsilosis	Fungi
25076_5_12	A01305	Infancy	Caesarean	25076_5_12_bin.8	8392011	98.21	GCA_000982555.2_CBS6318.1	13050515	64.36	0.00	98.85	Candida parapsilosis	Fungi
22178_5_5	B02098	Neonatal	Caesarean	22178_5_5_bin.3	231943	99.42	GCA_000982555.2_CBS6318.1	13050515	1.78	0.15	99.82	Candida parapsilosis	Fungi
24469_1_20	B01712	Infancy	Caesarean	24469_1_20_bin.1	13672161	98.91	GCA_000633855.1_ASM63385v1	15326821	91.88	0.00	99.08	Candida tropicalis	Fungi
24211_3_18	B01786	Neonatal	Vaginal	24211_3_18_bin.5	11905323	99.05	GCA_003675595.1_S18_1	11927748	98.07	0.01	97.78	Clavispora lusitaniae	Fungi
22178_4_22	B01954	Neonatal	Caesarean	22178_4_22_bin.9	11754852	99.25	GCA_003675595.1_S18_1	11927748	97.43	0.01	97.68	Clavispora lusitaniae	Fungi
24211_5_14	B02159	Neonatal	Caesarean	24211_5_14_bin.10	11600985	99.1	GCA_004026375.1_ASM402637v1	11907650	96.51	0.02	98.41	Clavispora lusitaniae	Fungi
21127_7_9	B01034	Neonatal	Caesarean	21127_7_9_bin.2	11104795	98.67	GCA_003675595.1_S18_1	11927748	91	0.01	99	Clavispora lusitaniae	Fungi
22178_4_23	B01954	Neonatal	Caesarean	22178_4_23_bin.8	8899691	98.39	GCA_004026375.1_ASM402637v1	11907650	74.16	0.02	97.43	Clavispora lusitaniae	Fungi
22178_4_21	B01954	Neonatal	Caesarean	22178_4_21_bin.7	7193482	98.08	GCA_004026375.1_ASM402637v1	11907650	59.84	0.02	97.23	Clavispora lusitaniae	Fungi
25076_5_3	C02056	Infancy	Caesarean	25076_5_3_bin.14	22594626	94.52	GCA_001402995.1_New2.3_080620	24836057	86.79	0.02	98.16	Geotrichum candidum	Fungi
25076_3_17	B01789	Infancy	Caesarean	25076_3_17_bin.17	18217115	91.21	GCA_001402995.1_New2.3_080620	24836057	68.45	0.02	97.47	Geotrichum candidum	Fungi
25076_4_7	C01392	Infancy	Caesarean	25076_4_7_bin.16	3489802	78.1	GCA_001402995.1_New2.3_080620	24836057	11.6	0.09	97.30	Geotrichum candidum	Fungi
25076_4_7	C01392	Infancy	Caesarean	25076_4_7_bin.8	1232830	90.58	GCA_001402995.1_New2.3_080620	24836057	4.59	0.12	97.85	Geotrichum candidum	Fungi
24759_5_17	B01719	Infancy	Vaginal	24759_5_17_bin.8	616429	86.9	GCA_001402995.1_New2.3_080620	24836057	2.53	0.16	95.33	Geotrichum candidum	Fungi
14795_54	521130	Adult	Vaginal	14795_54_bin.48	7991965	99.12	GCA_001651215.1_ASM165121v1	16468307	54.57	0.03	98.23	Blastocystis sp.	Protozoa
24469_1_12	B02257	Infancy	Vaginal	24469_1_12_bin.11	9957673	93.6	GCA_001660455.1_run3	11537868	82.26	0.01	98.97	Kluyveromyces marxianus	Fungi
24469_1_1	A01678	Infancy	Vaginal	24469_1_1_bin.4	13793901	97.1	GCA_000149685.1_ASM14968v1	15547272	86.6	0.02	95.55	Lodderomyces elongisporus	Fungi
22178_6_8	C01700	Neonatal	Caesarean	22178_6_8_bin.4	32973367	99.71	GCA_000697255.1_MucRacB9645-1.	65533039	64.45	0.01	99.78	Mucor racemosus	Fungi
22178_6_8	C01700	Neonatal	Caesarean	22178_6_8_bin.13	300816	99.91	GCA_000697255.1_MucRacB9645-1.	65533039	4.88	0.24	99.75	Mucor racemosus	Fungi
23430_6_21	B02263	Neonatal	Vaginal	23430_6_21_bin.3	13389706	98.49	GCA_001074275.1_ASM107427v1	13985759	93.61	0.01	99.04	Naumovozyma dairenensis	Fungi
21127_7_13	B01042	Neonatal	Caesarean	21127_7_13_bin.3	491140	94.37	GCA_000513335.1_PCAMFM013_20	35011981	1.36	0.18	97.88	Penicillium camemberti	Fungi
22178_6_4	C01695	Neonatal	Caesarean	22178_6_4_bin.9	6059083	94.19	GCA_001939915.1_ASM193991v1	26071999	22.29	0.06	97.82	Penicillium roqueforti	Fungi
21842_3_3	B01572	Neonatal	Vaginal	21842_3_3_bin.10	30145751	98.88	GCA_001750005.1_ASM175000v1	31778960	94.54	0.04	99.84	Penicillium solitum	Fungi
20596_5_19	B00046	Neonatal	Vaginal	20596_5_19_bin.7	10642991	95.91	GCA_001750005.1_ASM175000v1	31778960	32.56	0.04	97.92	Penicillium solitum	Fungi
18403_1	S1	Neonatal	Vaginal	18403_1_bin.8	5652925	92.66	GCA_001750005.1_ASM175000v1	31778960	16.73	0.06	97.89	Penicillium solitum	Fungi
24211_6_15	A02080	Neonatal	Caesarean	24211_6_15_bin.2	670327	67.16	GCA_001750005.1_ASM175000v1	31778960	1.42	0.20	98.10	Penicillium solitum	Fungi
21842_3_3	B01572	Neonatal	Vaginal	21842_3_3_bin.18	202305	99.94	GCA_001750005.1_ASM175000v1	31778960	0.55	0.26	99.83	Penicillium solitum	Fungi
21842_4_4	C01528	Neonatal	Caesarean	21842_4_4_bin.7	28127258	98.38	GCA_003800495.1_ASM380049v1	32063379	86.73	0.01	99	Penicillium sp.	Fungi
24469_3_19	C02190	Infancy	Caesarean	24469_3_19_bin.17	6690968	93.29	GCA_003339355.1_UCD_Pferm_PL1	10568644	59.16	0.03	97.3	Pichia fermentans	Fungi
24469_2_19	B02542	Infancy	Vaginal	24469_2_19_bin.16	9904781	98.1	GCA_003327685.1_ASM332768v1	12399968	90.84	0.01	97.78	Pichia kluyveri	Fungi
21242_4	A01166	Neonatal	Caesarean	21242_4_bin.4	9899929	98.02	GCA_003327685.1_ASM332768v1	12399968	90.56	0.01	97.96	Pichia kluyveri	Fungi
21127_7_8	C01075	Neonatal	Vaginal	21127_7_8_bin.4	4950115	70.16	GCA_002893375.1_ASM289337v1	37400776	9.28	0.09	98.41	Cyclospora cayetanensis	Protozoa
21842_4_18	C01752	Adult	Vaginal	21842_4_18_bin.9	4488229	75.74	GCA_002893375.1_ASM289337v1	37400776	9.11	0.09	98.56	Cyclospora cayetanensis	Protozoa
20727_4_3	B00085	Neonatal	Caesarean	20727_4_3_bin.24	4586269	72.06	GCA_002893375.1_ASM289337v1	37400776	8.85	0.10	98.49	Cyclospora cayetanensis	Protozoa
24469_4_19	C01873	Adult	Vaginal	24469_4_19_bin.30	4789869	69.94	GCA_002893375.1_ASM289337v1	37400776	8.84	0.09	98.45	Cyclospora cayetanensis	Protozoa
20727_6_5	B00139	Adult	Caesarean	20727_6_5_bin.8	4438575	74.26	GCA_002893375.1_ASM289337v1	37400776	8.81	0.09	98.44	Cyclospora cayetanensis	Protozoa
23584_5_6	A02913	Adult	Caesarean	23584_5_6_bin.47	4528414	72.52	GCA_002893375.1_ASM289337v1	37400776	8.75	0.10	98.53	Cyclospora cayetanensis	Protozoa
23164_6_4	B01423	Neonatal	Vaginal	23164_6_4_bin.23	4342922	75.41	GCA_002893375.1_ASM289337v1	37400776	8.74	0.09	98.47	Cyclospora cayetanensis	Protozoa
23584_5_22	B02243	Adult	Vaginal	23584_5_22_bin.47	4589769	71.06	GCA_002893375.1_ASM289337v1	37400776	8.72	0.09	98.34	Cyclospora cayetanensis	Protozoa
22178_7_2	C01994	Neonatal	Vaginal	22178_7_2_bin.21	4331560	75.1	GCA_002893375.1_ASM289337v1	37400776	8.72	0.10	98.31	Cyclospora cayetanensis	Protozoa
24469_2_1	B01791	Infancy	Vaginal	24469_2_1_bin.40	4141262	78.37	GCA_002893375.1_ASM289337v1	37400776	8.67	0.10	98.49	Cyclospora cayetanensis	Protozoa
19646_4_2	BBS0067	Adult	Vaginal	19646_4_2_bin.19	4251193	76.1	GCA_002893375.1_ASM289337v1	37400776	8.65	0.09	98.57	Cyclospora cayetanensis	Protozoa
21673_20	C01443	Adult	Caesarean	21673_20_bin.18	4242859	75.72	GCA_002893375.1_ASM289337v1	37400776	8.61	0.09	98.64	Cyclospora cayetanensis	Protozoa
20727_7_7	A00163	Adult	Vaginal	20727_7_7_bin.73	4030958	79.51	GCA_002893375.1_ASM289337v1	37400776	8.59	0.10	98.56	Cyclospora cayetanensis	Protozoa
21989_7_8	B01772	Adult	Caesarean	21989_7_8_bin.8	4281472	74.79	GCA_002893375.1_ASM289337v1	37400776	8.55	0.10	98.23	Cyclospora cayetanensis	Protozoa
23430_8_21	A02872	Adult	Caesarean	23430_8_21_bin.4	4166716	76.31	GCA_002893375.1_ASM289337v1	37400776	8.49	0.10	98.49	Cyclospora cayetanensis	Protozoa
21999_4_8	C01917	Adult	Vaginal	21999_4_8_bin.3	4485250	70.8	GCA_002893375.1_ASM289337v1	37400776	8.48	0.10	98.32	Cyclospora cayetanensis	Protozoa
21242_18	B01194	Adult	Vaginal	21242_18_bin.24	4015066	77.74	GCA_002893375.1_ASM289337v1	37400776	8.34	0.10	98.66	Cyclospora cayetanensis	Protozoa
21242_20	C01201	Adult	Vaginal	21242_20_bin.43	4292864	72.71	GCA_002893375.1_ASM289337v1	37400776	8.32	0.10	98.27	Cyclospora cayetanensis	Protozoa
23164_6_7	C01756	Adult	Caesarean	23164_6_7_bin.2	4707987	69.5	GCA_002893375.1_ASM289337v1	37400776	8.31	0.10	98.45	Cyclospora cayetanensis	Protozoa
24469_4_1	A01015	Adult	Caesarean	24469_4_1_bin.50	4010776	77.24	GCA_002893375.1_ASM289337v1	37400776	8.28	0.10	98.44	Cyclospora cayetanensis	Protozoa
21242_36	B01277	Adult	Vaginal	21242_36_bin.57	3756493	82.39	GCA_002893375.1_ASM289337v1	37400776	8.28	0.10	98.54	Cyclospora cayetanensis	Protozoa
24469_1_20	B01712	Infancy	Caesarean	24469_1_20_bin.9	7287270	69.51	GCA_000286515.1_ASM28651v1	10448518	48.9	0.03	98.37	Pichia kudriavzevii	Fungi
20727_6_10	B00145	Neonatal	Vaginal	20727_6_10_bin.11	4660015	65.97	GCA_002893375.1_ASM289337v1	37400776	8.22	0.10	97.99	Cyclospora cayetanensis	Protozoa
23430_8_10	C02514	Adult	Vaginal	23430_8_10_bin.39	4465037	68.93	GCA_002893375.1_ASM289337v1	37400776	8.22	0.10	98.22	Cyclospora cayetanensis	Protozoa
21842_3_20	B01716	Adult	Vaginal	21842_3_20_bin.32	4338043	70.89	GCA_002893375.1_ASM289337v1	37400776	8.2	0.10	98.22	Cyclospora cayetanensis	Protozoa
24759_5_2	C02061	Neonatal	Vaginal	24759_5_2_bin.1	4118001	73.94	GCA_002893375.1_ASM289337v1	37400776	8.16	0.09	98.41	Cyclospora cayetanensis	Protozoa
21127_7_15	C01007	Neonatal	Vaginal	21127_7_15_bin.2	3840127	79.16	GCA_002893375.1_ASM289337v1	37400776	8.13	0.10	98.54	Cyclospora cayetanensis	Protozoa
24469_5_12	B02159	Adult	Caesarean	24469_5_12_bin.8	4381490	70.79	GCA_002893375.1_ASM289337v1	37400776	8.08	0.10	98.57	Cyclospora cayetanensis	Protozoa
24469_2_5	B02416	Infancy	Vaginal	24469_2_5_bin.3	4159535	72.62	GCA_002893375.1_ASM289337v1	37400776	8.08	0.10	98.29	Cyclospora cayetanensis	Protozoa
21127_6_6	C01007	Neonatal	Vaginal	21127_6_6_bin.20	3581609	84.28	GCA_002893375.1_ASM289337v1	37400776	8.07	0.09	98.63	Cyclospora cayetanensis	Protozoa
21999_3_7	C01839	Adult	Vaginal	21999_3_7_bin.34	3945597	76.28	GCA_002893375.1_ASM289337v1	37400776	8.05	0.10	98.65	Cyclospora cayetanensis	Protozoa
21842_2_11	A01763	Adult	Vaginal	21842_2_11_bin.34	3770616	79.64	GCA_002893375.1_ASM289337v1	37400776	8.03	0.10	98.67	Cyclospora cayetanensis	Protozoa
21999_4_12	C01919	Adult	Caesarean	21999_4_12_bin.23	4040666	74.31	GCA_002893375.1_ASM289337v1	37400776	8.03	0.10	98.49	Cyclospora cayetanensis	Protozoa
18403_21	BBS0006	Neonatal	Vaginal	18403_21_bin.22	4247161	72.05	GCA_002893375.1_ASM289337v1	37400776	8.01	0.10	97.83	Cyclospora cayetanensis	Protozoa
21999_3_4	C01839	Neonatal	Vaginal	21999_3_4_bin.17	3663004	81.77	GCA_002893375.1_ASM289337v1	37400776	8.01	0.10	98.15	Cyclospora cayetanensis	Protozoa
23584_5_19	C02131	Adult	Vaginal	23584_5_19_bin.32	3886991	76.61	GCA_002893375.1_ASM289337v1	37400776	7.96	0.10	98.53	Cyclospora cayetanensis	Protozoa

21242_82	C01012	Adult	Caesarean	21242_82_bin.3	3899369	76.18	GCA_002893375.1_ASM289337v1	37400776	7.95	0.10	98.64	Cyclospora cayetanensis	Protozoa
23430_8_20	C02756	Adult	Caesarean	23430_8_20_bin.29	4395380	67.6	GCA_002893375.1_ASM289337v1	37400776	7.94	0.11	98.03	Cyclospora cayetanensis	Protozoa
24469_5_13	A02193	Adult	Vaginal	24469_5_13_bin.16	4151361	71.21	GCA_002893375.1_ASM289337v1	37400776	7.92	0.11	98.31	Cyclospora cayetanensis	Protozoa
25076_7_10	B02885	Infancy	Vaginal	25076_7_10_bin.18	4251791	69.67	GCA_002893375.1_ASM289337v1	37400776	7.92	0.11	98.09	Cyclospora cayetanensis	Protozoa
25076_7_18	B02274	Infancy	Caesarean	25076_7_18_bin.27	3719354	79.54	GCA_002893375.1_ASM289337v1	37400776	7.91	0.10	98.41	Cyclospora cayetanensis	Protozoa
24469_3_18	B01626	Infancy	Vaginal	24469_3_18_bin.20	3544810	83.05	GCA_002893375.1_ASM289337v1	37400776	7.88	0.10	98.67	Cyclospora cayetanensis	Protozoa
21242_50	C01381	Adult	Vaginal	21242_50_bin.29	3929779	75.04	GCA_002893375.1_ASM289337v1	37400776	7.87	0.11	98.55	Cyclospora cayetanensis	Protozoa
21673_2	C01390	Adult	Caesarean	21673_2_bin.7	3579333	82.09	GCA_002893375.1_ASM289337v1	37400776	7.87	0.10	98.53	Cyclospora cayetanensis	Protozoa
21242_7	C01070	Neonatal	Vaginal	21242_7_bin.15	3492194	84.03	GCA_002893375.1_ASM289337v1	37400776	7.85	0.11	98.35	Cyclospora cayetanensis	Protozoa
23430_8_13	C02548	Adult	Vaginal	23430_8_13_bin.10	3847707	76.17	GCA_002893375.1_ASM289337v1	37400776	7.84	0.10	98.44	Cyclospora cayetanensis	Protozoa
21242_15	C01204	Neonatal	Vaginal	21242_15_bin.10	4022126	72.51	GCA_002893375.1_ASM289337v1	37400776	7.83	0.11	98.05	Cyclospora cayetanensis	Protozoa
21999_3_15	C01841	Adult	Vaginal	21999_3_15_bin.51	3595033	81.45	GCA_002893375.1_ASM289337v1	37400776	7.83	0.10	98.59	Cyclospora cayetanensis	Protozoa
19646_4_12	S13	Adult	Vaginal	19646_4_12_bin.31	3627336	80.55	GCA_002893375.1_ASM289337v1	37400776	7.82	0.10	98.41	Cyclospora cayetanensis	Protozoa
14795_55	519129	Adult	Caesarean	14795_55_bin.4	3635592	80.95	GCA_002893375.1_ASM289337v1	37400776	7.77	0.10	98.86	Cyclospora cayetanensis	Protozoa
25076_4_20	C01840	Infancy	Vaginal	25076_4_20_bin.16	3789472	76.42	GCA_002893375.1_ASM289337v1	37400776	7.74	0.10	98.46	Cyclospora cayetanensis	Protozoa
21242_21	C01204	Adult	Vaginal	21242_21_bin.40	3592916	79.52	GCA_002893375.1_ASM289337v1	37400776	7.62	0.10	98.78	Cyclospora cayetanensis	Protozoa
20727_5_3	A00134	Adult	Caesarean	20727_5_3_bin.4	3929889	72.44	GCA_002893375.1_ASM289337v1	37400776	7.61	0.10	98.09	Cyclospora cayetanensis	Protozoa
21127_7_11	C01138	Adult	Caesarean	21127_7_11_bin.34	3449460	82.56	GCA_002893375.1_ASM289337v1	37400776	7.61	0.10	98.71	Cyclospora cayetanensis	Protozoa
21842_2_17	B01472	Neonatal	Caesarean	21842_2_17_bin.2	7500649	97.69	GCA_000931965.1_ASM93196v1	19981819	37.37	0.04	96.89	Rhodotorula mucilaginosa	Fungi
24469_5_3	C01959	Adult	Caesarean	24469_5_3_bin.2	3627186	78.11	GCA_002893375.1_ASM289337v1	37400776	7.59	0.10	98.17	Cyclospora cayetanensis	Protozoa
23584_5_20	C02143	Adult	Vaginal	23584_5_20_bin.32	3452290	81.9	GCA_002893375.1_ASM289337v1	37400776	7.56	0.10	98.56	Cyclospora cayetanensis	Protozoa
14795_56	513122	Adult	Vaginal	14795_56_bin.55	3882978	72.74	GCA_002893375.1_ASM289337v1	37400776	7.55	0.10	98.78	Cyclospora cayetanensis	Protozoa
22178_7_1	C01991	Adult	Vaginal	22178_7_1_bin.24	3607337	77.98	GCA_002893375.1_ASM289337v1	37400776	7.5	0.10	98.88	Cyclospora cayetanensis	Protozoa
24469_5_9	C02056	Adult	Caesarean	24469_5_9_bin.25	3715335	75.55	GCA_002893375.1_ASM289337v1	37400776	7.46	0.10	98.45	Cyclospora cayetanensis	Protozoa
22178_3_17	A02064	Adult	Caesarean	22178_3_17_bin.13	4863862	62.07	GCA_002893375.1_ASM289337v1	37400776	7.45	0.11	98.22	Cyclospora cayetanensis	Protozoa
22607_3_9	B02249	Neonatal	Vaginal	22607_3_9_bin.6	3494449	79.39	GCA_002893375.1_ASM289337v1	37400776	7.45	0.10	97.93	Cyclospora cayetanensis	Protozoa
14794_1	521130	Neonatal	Vaginal	14794_1_bin.3	3198437	86.97	GCA_002893375.1_ASM289337v1	37400776	7.43	0.10	98.81	Cyclospora cayetanensis	Protozoa
25076_2_23	B02861	Neonatal	Vaginal	25076_2_23_bin.4	3507778	79.26	GCA_002893375.1_ASM289337v1	37400776	7.42	0.10	98.04	Cyclospora cayetanensis	Protozoa
21127_6_20	B01042	Adult	Caesarean	21127_6_20_bin.27	3881957	71.26	GCA_002893375.1_ASM289337v1	37400776	7.4	0.11	98.02	Cyclospora cayetanensis	Protozoa
23430_8_4	C02142	Adult	Caesarean	23430_8_4_bin.44	3227090	85.19	GCA_002893375.1_ASM289337v1	37400776	7.35	0.10	98.55	Cyclospora cayetanensis	Protozoa
23584_5_9	C01914	Adult	Caesarean	23584_5_9_bin.36	4931269	60.35	GCA_002893375.1_ASM289337v1	37400776	7.33	0.11	98.06	Cyclospora cayetanensis	Protozoa
25013_2_23	B02528	Infancy	Vaginal	25013_2_23_bin.6	3587592	75.82	GCA_002893375.1_ASM289337v1	37400776	7.28	0.10	98.28	Cyclospora cayetanensis	Protozoa
21242_59	B01261	Neonatal	Vaginal	21242_59_bin.1	3288406	82.51	GCA_002893375.1_ASM289337v1	37400776	7.27	0.10	98.27	Cyclospora cayetanensis	Protozoa
24469_5_6	C02061	Adult	Vaginal	24469_5_6_bin.32	3463089	78.41	GCA_002893375.1_ASM289337v1	37400776	7.25	0.10	98.49	Cyclospora cayetanensis	Protozoa
21842_3_23	B01719	Adult	Vaginal	21842_3_23_bin.46	4566119	63.76	GCA_002893375.1_ASM289337v1	37400776	7.22	0.10	98.31	Cyclospora cayetanensis	Protozoa
21523_4_2	A01563	Adult	Caesarean	21523_4_2_bin.19	3254524	82.86	GCA_002893375.1_ASM289337v1	37400776	7.2	0.11	98.25	Cyclospora cayetanensis	Protozoa
20596_5_17	B00046	Adult	Vaginal	20596_5_17_bin.70	3310806	81	GCA_002893375.1_ASM289337v1	37400776	7.19	0.11	98.43	Cyclospora cayetanensis	Protozoa
19646_5_6	BBS0024	Adult	Caesarean	19646_5_6_bin.52	3403186	78.66	GCA_002893375.1_ASM289337v1	37400776	7.17	0.10	98.34	Cyclospora cayetanensis	Protozoa
14795_61	604136	Adult	Vaginal	14795_61_bin.83	3323353	80.57	GCA_002893375.1_ASM289337v1	37400776	7.15	0.10	98.87	Cyclospora cayetanensis	Protozoa
22178_5_19	B02147	Neonatal	Vaginal	22178_5_19_bin.12	3249522	81.19	GCA_002893375.1_ASM289337v1	37400776	7.06	0.10	98.33	Cyclospora cayetanensis	Protozoa
20596_4_6	B00004	Adult	Vaginal	20596_4_6_bin.67	3131047	83.22	GCA_002893375.1_ASM289337v1	37400776	6.95	0.11	98.67	Cyclospora cayetanensis	Protozoa
23584_4_23	C02649	Adult	Vaginal	23584_4_23_bin.35	3836394	67.47	GCA_002893375.1_ASM289337v1	37400776	6.92	0.12	96.4	Cyclospora cayetanensis	Protozoa
21673_58	B01368	Adult	Vaginal	21673_58_bin.37	3161371	79.6	GCA_002893375.1_ASM289337v1	37400776	6.75	0.10	97.7	Cyclospora cayetanensis	Protozoa
14794_4	521130	Neonatal	Vaginal	14794_4_bin.5	3122966	77.9	GCA_002893375.1_ASM289337v1	37400776	6.52	0.11	98.62	Cyclospora cayetanensis	Protozoa
22178_5_7	B02098	Adult	Caesarean	22178_5_7_bin.45	3030006	79.29	GCA_002893375.1_ASM289337v1	37400776	6.44	0.11	98.05	Cyclospora cayetanensis	Protozoa
20727_5_9	B00146	Neonatal	Vaginal	20727_5_9_bin.2	3094540	76.48	GCA_002893375.1_ASM289337v1	37400776	6.33	0.11	98.37	Cyclospora cayetanensis	Protozoa
21127_6_14	C01052	Adult	Vaginal	21127_6_14_bin.57	3588918	65.74	GCA_002893375.1_ASM289337v1	37400776	6.29	0.11	97.72	Cyclospora cayetanensis	Protozoa
24211_6_4	B02382	Neonatal	Vaginal	24211_6_4_bin.4	3286345	77	GCA_002893375.1_ASM289337v1	37400776	6.27	0.11	98.16	Cyclospora cayetanensis	Protozoa
21673_30	B01364	Neonatal	Vaginal	21673_30_bin.22	3196398	72.34	GCA_002893375.1_ASM289337v1	37400776	6.21	0.11	97.65	Cyclospora cayetanensis	Protozoa
24469_4_5	C01485	Adult	Vaginal	24469_4_5_bin.15	2830473	81.95	GCA_002893375.1_ASM289337v1	37400776	6.21	0.11	98.51	Cyclospora cayetanensis	Protozoa
14801_42	515126	Neonatal	Vaginal	14801_42_bin.6	2694022	85.74	GCA_002893375.1_ASM289337v1	37400776	6.19	0.11	98.36	Cyclospora cayetanensis	Protozoa
20727_5_17	A00106	Adult	Vaginal	20727_5_17_bin.17	3048024	74.74	GCA_002893375.1_ASM289337v1	37400776	6.1	0.11	98.16	Cyclospora cayetanensis	Protozoa
21999_4_24	C01990	Adult	Vaginal	21999_4_24_bin.19	2862322	79.51	GCA_002893375.1_ASM289337v1	37400776	6.09	0.11	98.55	Cyclospora cayetanensis	Protozoa
25076_6_16	B02752	Infancy	Vaginal	25076_6_16_bin.10	2961884	75.81	GCA_002893375.1_ASM289337v1	37400776	6.01	0.11	98.62	Cyclospora cayetanensis	Protozoa
24469_6_22	B02166	Infancy	Caesarean	24469_6_22_bin.12	3000019	74.66	GCA_002893375.1_ASM289337v1	37400776	6	0.12	96.43	Cyclospora cayetanensis	Protozoa
24469_7_4	B01408	Infancy	Vaginal	24469_7_4_bin.13	4522438	73.92	GCA_002893375.1_ASM289337v1	37400776	5.99	0.12	96.91	Cyclospora cayetanensis	Protozoa
21127_5_11	A00942	Adult	Vaginal	21127_5_11_bin.39	2807368	79.34	GCA_002893375.1_ASM289337v1	37400776	5.95	0.12	98.34	Cyclospora cayetanensis	Protozoa
19646_5_3	BBS0014	Neonatal	Vaginal	19646_5_3_bin.10	2867961	76.54	GCA_002893375.1_ASM289337v1	37400776	5.87	0.11	98.61	Cyclospora cayetanensis	Protozoa
14794_2	521130	Neonatal	Vaginal	14794_2_bin.2	2856877	75.83	GCA_002893375.1_ASM289337v1	37400776	5.8	0.12	98.57	Cyclospora cayetanensis	Protozoa
25076_7_19	B02935	Infancy	Vaginal	25076_7_19_bin.4	2829942	75.95	GCA_002893375.1_ASM289337v1	37400776	5.77	0.11	98.62	Cyclospora cayetanensis	Protozoa
24211_2_17	B01626	Neonatal	Vaginal	24211_2_17_bin.2	2516393	85.42	GCA_002893375.1_ASM289337v1	37400776	5.76	0.11	98.18	Cyclospora cayetanensis	Protozoa
21127_4_10	A00541	Neonatal	Vaginal	21127_4_10_bin.3	2741962	76.56	GCA_002893375.1_ASM289337v1	37400776	5.58	0.11	98.43	Cyclospora cayetanensis	Protozoa
21242_52	B01364	Adult	Vaginal	21242_52_bin.3	4397611	69.74	GCA_002893375.1_ASM289337v1	37400776	5.37	0.14	94.28	Cyclospora cayetanensis	Protozoa
25076_3_24	B02320_T1	Infancy	Vaginal	25076_3_24_bin.11	3114463	65.17	GCA_002893375.1_ASM289337v1	37400776	5.36	0.13	97.03	Cyclospora cayetanensis	Protozoa
24469_5_9	C02056	Adult	Caesarean	24469_5_9_bin.3	2470956	80.59	GCA_002893375.1_ASM289337v1	37400776	5.34	0.14	94.8	Cyclospora cayetanensis	Protozoa
24469_3_4	B01299	Infancy	Vaginal	24469_3_4_bin.47	2328753	84.77	GCA_002893375.1_ASM289337v1	37400776	5.27	0.12	97.42	Cyclospora cayetanensis	Protozoa
14795_58	606141	Adult	Caesarean	14795_58_bin.17	2464353	79.44	GCA_002893375.1_ASM289337v1	37400776	5.25	0.12	98.56	Cyclospora cayetanensis	Protozoa
19646_4_5	BBS0070	Adult	Caesarean	19646_4_5_bin.36	2168566	89.41	GCA_002893375.1_ASM289337v1	37400776	5.21	0.12	97.5	Cyclospora cayetanensis	Protozoa
24469_2_6	B01450_T1	Infancy	Caesarean	24469_2_6_bin.1	2073911	92.4	GCA_002893375.1_ASM289337v1	37400776	5.18	0.12	97.56	Cyclospora cayetanensis	Protozoa
22178_7_16	C02047	Adult	Caesarean	22178_7_16_bin.11	578666	97.72	GCA_000743755.1_ASM74375v1	12919355	5.18	0.12	97.61	Blastocystis sp.	Protozoa
24469_4_14	B01771	Neonatal	Vaginal	24469_4_14_bin.10	2691533	71.86	GCA_002893375.1_ASM289337v1	37400776	5.17	0.11	98.69	Cyclospora cayetanensis	Protozoa
14795_54	521130	Adult	Vaginal	14795_54_bin.32	2462003	78.25	GCA_002893375.1_ASM289337v1	37400776	5.12	0.13	98.32	Cyclospora cayetanensis	Protozoa
24469_7_20	C01844	Infancy	Vaginal	24469_7_20_bin.9	2387412	79.52	GCA_002893375.1_ASM289337v1	37400776	5.1	0.12	97.82	Cyclospora cayetanensis	Protozoa
20727_5_8	B00146	Neonatal	Vaginal	20727_5_8_bin.20	2450530	76.26	GCA_002893375.1_ASM289337v1	37400776	5.01	0.13	98.41	Cyclospora cayetanensis	Protozoa
21127_7_23	B01022	Adult	Vaginal	21127_7_23_bin.15	3546715	70.11	GCA_002893375.1_ASM289337v1	37400776	4.93	0.15	93.76	Cyclospora cayetanensis	Protozoa
20727_5_10	B00146	Neonatal	Vaginal	20727_5_10_bin.14	2380497	76.78	GCA_002893375.1_ASM289337v1	37400776	4.9	0.13	98.46	Cyclospora cayetanensis	Protozoa
25013_4_4	C02411	Neonatal	Vaginal	25013_4_4_bin.1	2433393	93.81	GCA_900178055.1_L719	2553819	90.3	0.01	98.98	Saccharomyces cerevisiae	Fungi
23584_5_13	B01947	Adult	Caesarean	23584_5_13_bin.59	2298124	78	GCA_002893375.1_ASM289337v1	37400776	4.81	0.12	98.61	Cyclospora cayetanensis	Protozoa
25013_3_21	C02130	Neonatal	Vaginal	25013_3_21_bin.8	2465075	72.2	GCA_002893375.1_ASM289337v1	37400776	4.79	0.12	97.54	Cyclospora cayetanensis	Protozoa
19646_5_1	BBS0006	Adult	Vaginal	19646_5_1_bin.38	2354893	75.58	GCA_002893375.1_ASM289337v1	37400776	4.77	0.14	96.32	Cyclospora cayetanensis	Protozoa
22178_5_3	B02005	Adult	Caesarean	22178_5_3_bin.49	1923611	91.53	GCA_002893375.1_ASM289337v1	37400776	4.75	0.13	97.53	Cyclospora cayetanensis	Protozoa
21673_3	C01389	Adult	Caesarean	21673_3_bin.2	1980548	89.02	GCA_002893375.1_ASM289337v1	37400776	4.71	0.13	97.69	Cyclospora cayetanensis	Protozoa
20727_5_3	A00134	Adult	Caesarean	20727_5_3_bin.37	2081244	83.67	GCA_002893375.1_ASM289337v1	37400776	4.7	0.14	94.58	Cyclospora cayetanensis	Protozoa
23430_8_14	C02634	Adult	Vaginal	23430_8_14_bin.7	1881621	93.24	GCA_002893375.1_ASM289337v1	37400776	4.7	0.13	97.86	Cyclospora cayetanensis	Protozoa
21999_4_24	C01990	Adult	Vaginal	21999_4_24_bin.6	1965715	88.5	GCA_002893375.1_ASM289337v1	37400776	4.67	0.14	96.65	Cyclospora cayetanensis	Protozoa
14795_60	515127	Adult	Vaginal	14795_60_bin.85	1973383	89.93	GCA_002893375.1_ASM289337v1	37400776	4.66	0.15	94.69	Cyclospora cayetanensis	Protozoa
21127_6_15	A01011	Adult	Vaginal	21127_6_15_bin.21	3141319	71.74	GCA_002893375.1_ASM289337v1	37400776	4.66	0.13	96.23	Cyclospora cayetanensis	Protozoa
23164_7_4	B02273	Adult	Vaginal	23164_7_4_bin.36	1908497	90.75	GCA_002893375.1_ASM289337v1	37400776	4.66	0.14	94.92	Cyclospora cayetanensis	Protozoa
25013_2_22	B01218	Infancy	Vaginal	25013_2_22_bin.2	1981605	87.83	GCA_002893375.1_ASM289337v1	37400776	4.63	0.16	94.85	Cyclospora cayetanensis	Protozoa
23584_5_22	B02243	Adult	Vaginal	23584_5_22_bin.54	3113371	70.11	GCA_002893375.1_ASM289337v1	37400776	4.59	0.15	94.19	Cyclospora cayetanensis	Protozoa
21242_13	A01173	Neonatal	Caesarean	21242_13_bin.1	2301674	97.58	GCA_900178055.1_L719	2553819	88.86	0.01	99.01	Saccharomyces cerevisiae	Fungi
24211_3_19	B01798	Neonatal	Vaginal	24211_3_19_bin.9	2120178	79.88	GCA_002893375.1_ASM289337v1	37400776	4.55	0.13	97.52	Cyclospora cayetanensis	Protozoa
20727_4_14	B00099	Adult	Vaginal	20727_4_14_bin.9	3538589	67.72	GCA_002893375.1_ASM289337v1	37400776	4.52	0.14	93.87	Cyclospora cayetanensis	Protozoa
21999_3_11	C01840	Adult	Vaginal	21999_3_11_bin.46	2300724	75.97	GCA_002893375.1_ASM289337v1	37400776	4.44	0.14	94.67	Cyclospora cayetanensis	Protozoa
20596_5_22	B00052	Neonatal	Vaginal	20596_5_22_bin.13	2199406	75.18	GCA_002893375.1_ASM289337v1	37400776	4.43	0.13	98.41	Cyclospora cayetanensis	Protozoa
21999_4_20	C01930	Adult	Caesarean	21999_4_20_bin.34	1979999	84.34	GCA_002893375.1_ASM289337v1	37400776	4.41	0.17	94.28	Cyclospora cayetanensis	Protozoa
23584_5_19	C02131	Adult	Vaginal	23584_5_19_bin.39	1903947	84.83	GCA_002893375.1_ASM289337v1	37400776	4.35	0.15	95.02	Cyclospora cayetanensis	Protozoa
24211_2_1	A01162	Neonatal	Vaginal	24211_2_1_bin.6	2201565	73.03	GCA_002893375.1_ASM289337v1	37400776	4.33	0.13	97.38	Cyclospora cayetanensis	Protozoa
21673_42	B00235	Neonatal	Vaginal	21673_42_bin.3	2417257	66.73	GCA_002893375.1_ASM289337v1	37400776	4.32	0.12	98.43	Cyclospora cayetanensis	Protozoa
20727_3_18	B00075	Adult	Caesarean	20727_3_18_bin.9	2996275	71.36	GCA_002893375.1_ASM289337v1	37400776	4.31	0.15	92.96	Cyclospora cayetanensis	Protozoa

24469_6_19	B01775	Infancy	Vaginal	24469_6_19_bin.8	3280947	69.02	GCA_002893375.1_ASM289337v1	37400776	4.3	0.15	93.19	Cyclospora cayetanensis	Protozoa
22178_6_17	C01871	Adult	Vaginal	22178_6_17_bin.12	1837818	88.24	GCA_002893375.1_ASM289337v1	37400776	4.29	0.15	94.3	Cyclospora cayetanensis	Protozoa
23430_8_12	C02565	Adult	Caesarean	23430_8_12_bin.35	1931254	84.35	GCA_002893375.1_ASM289337v1	37400776	4.26	0.16	94.65	Cyclospora cayetanensis	Protozoa
19646_4_17	S34	Adult	Vaginal	19646_4_17_bin.22	3127355	68.96	GCA_002893375.1_ASM289337v1	37400776	4.24	0.15	93.41	Cyclospora cayetanensis	Protozoa
21127_5_11	A00942	Adult	Vaginal	21127_5_11_bin.37	1855011	85.86	GCA_002893375.1_ASM289337v1	37400776	4.2	0.16	94.58	Cyclospora cayetanensis	Protozoa
14795_60	515127	Adult	Vaginal	14795_60_bin.55	1977711	79.38	GCA_002893375.1_ASM289337v1	37400776	4.18	0.13	98.47	Cyclospora cayetanensis	Protozoa
24469_4_10	B01710	Neonatal	Vaginal	24469_4_10_bin.9	2055116	75.1	GCA_002893375.1_ASM289337v1	37400776	4.16	0.14	97.6	Cyclospora cayetanensis	Protozoa
14795_60	515127	Adult	Vaginal	14795_60_bin.76	1858550	82.09	GCA_002893375.1_ASM289337v1	37400776	4.14	0.17	90.35	Cyclospora cayetanensis	Protozoa
24469_2_17	B01572	Infancy	Vaginal	24469_2_17_bin.9	1659668	90.87	GCA_002893375.1_ASM289337v1	37400776	4.12	0.13	96.88	Cyclospora cayetanensis	Protozoa
20727_4_14	B00099	Adult	Vaginal	20727_4_14_bin.66	1914784	79.11	GCA_002893375.1_ASM289337v1	37400776	4.09	0.19	90.39	Cyclospora cayetanensis	Protozoa
24469_1_18	B01797	Infancy	Vaginal	24469_1_18_bin.11	1869741	79.6	GCA_002893375.1_ASM289337v1	37400776	4.09	0.16	94.61	Cyclospora cayetanensis	Protozoa
23584_5_12	B01891	Adult	Vaginal	23584_5_12_bin.38	1955342	83.95	GCA_002893375.1_ASM289337v1	37400776	4.08	0.19	90.43	Cyclospora cayetanensis	Protozoa
23430_8_20	C02756	Adult	Caesarean	23430_8_20_bin.7	2642194	83.14	GCA_002893375.1_ASM289337v1	37400776	3.98	0.15	94.5	Cyclospora cayetanensis	Protozoa
23584_5_13	B01947	Adult	Caesarean	23584_5_13_bin.65	1979618	75.08	GCA_002893375.1_ASM289337v1	37400776	3.97	0.12	98.48	Cyclospora cayetanensis	Protozoa
21127_4_6	B00537	Adult	Vaginal	21127_4_6_bin.17	1710464	84.55	GCA_002893375.1_ASM289337v1	37400776	3.92	0.19	90.67	Cyclospora cayetanensis	Protozoa
23430_8_20	C02756	Adult	Caesarean	23430_8_20_bin.39	1780609	81.7	GCA_002893375.1_ASM289337v1	37400776	3.92	0.19	90.25	Cyclospora cayetanensis	Protozoa
25013_1_14	B02607	Neonatal	Vaginal	25013_1_14_bin.19	2106515	68.41	GCA_002893375.1_ASM289337v1	37400776	3.87	0.14	97.48	Cyclospora cayetanensis	Protozoa
14795_55	519129	Adult	Caesarean	14795_55_bin.8	1868613	81.48	GCA_002893375.1_ASM289337v1	37400776	3.83	0.18	94.17	Cyclospora cayetanensis	Protozoa
24469_4_14	B01771	Neonatal	Vaginal	24469_4_14_bin.2	1879524	75.77	GCA_002893375.1_ASM289337v1	37400776	3.81	0.14	98.38	Cyclospora cayetanensis	Protozoa
23584_5_19	C02131	Adult	Vaginal	23584_5_19_bin.51	1637272	86.21	GCA_002893375.1_ASM289337v1	37400776	3.81	0.19	90.27	Cyclospora cayetanensis	Protozoa
21127_6_20	B01042	Adult	Caesarean	21127_6_20_bin.24	1752902	80.16	GCA_002893375.1_ASM289337v1	37400776	3.8	0.19	89.74	Cyclospora cayetanensis	Protozoa
24759_5_15	B01236	Infancy	Caesarean	24759_5_15_bin.26	1838139	79.05	GCA_002893375.1_ASM289337v1	37400776	3.79	0.15	96.31	Cyclospora cayetanensis	Protozoa
24469_5_8	A02080	Adult	Caesarean	24469_5_8_bin.52	1654443	84.67	GCA_002893375.1_ASM289337v1	37400776	3.76	0.20	90.68	Cyclospora cayetanensis	Protozoa
21127_5_12	A00940	Adult	Vaginal	21127_5_12_bin.54	1480248	94.54	GCA_002893375.1_ASM289337v1	37400776	3.75	0.15	97.81	Cyclospora cayetanensis	Protozoa
23430_8_1	C02186	Adult	Vaginal	23430_8_1_bin.57	1657872	83.28	GCA_002893375.1_ASM289337v1	37400776	3.75	0.18	90.72	Cyclospora cayetanensis	Protozoa
14795_56	513122	Adult	Vaginal	14795_56_bin.68	1710005	79.9	GCA_002893375.1_ASM289337v1	37400776	3.68	0.20	90.31	Cyclospora cayetanensis	Protozoa
14795_60	515127	Adult	Vaginal	14795_60_bin.82	2329095	72.45	GCA_002893375.1_ASM289337v1	37400776	3.59	0.12	97.82	Cyclospora cayetanensis	Protozoa
21999_3_19	C01844	Adult	Vaginal	21999_3_19_bin.24	1639041	79.82	GCA_002893375.1_ASM289337v1	37400776	3.56	0.19	90.1	Cyclospora cayetanensis	Protozoa
25076_7_19	B02935	Infancy	Vaginal	25076_7_19_bin.20	1738692	74.96	GCA_002893375.1_ASM289337v1	37400776	3.5	0.15	98.64	Cyclospora cayetanensis	Protozoa
23430_8_3	C02223	Adult	Caesarean	23430_8_3_bin.14	1551611	83.88	GCA_002893375.1_ASM289337v1	37400776	3.49	0.18	94.34	Cyclospora cayetanensis	Protozoa
19646_4_13	S3	Adult	Vaginal	19646_4_13_bin.9	1768224	73.1	GCA_002893375.1_ASM289337v1	37400776	3.48	0.19	89.72	Cyclospora cayetanensis	Protozoa
20727_5_8	B00146	Neonatal	Vaginal	20727_5_8_bin.7	1733808	74.13	GCA_002893375.1_ASM289337v1	37400776	3.45	0.13	98.5	Cyclospora cayetanensis	Protozoa
21127_6_21	B01039	Adult	Vaginal	21127_6_21_bin.45	2455346	68.47	GCA_002893375.1_ASM289337v1	37400776	3.45	0.17	90.8	Cyclospora cayetanensis	Protozoa
25076_5_15	B01848	Infancy	Caesarean	25076_5_15_bin.10	1469677	86.04	GCA_002893375.1_ASM289337v1	37400776	3.44	0.16	94.25	Cyclospora cayetanensis	Protozoa
22178_7_3	C01994	Neonatal	Vaginal	22178_7_3_bin.4	1765918	71.45	GCA_002893375.1_ASM289337v1	37400776	3.41	0.14	97.33	Cyclospora cayetanensis	Protozoa
24469_5_6	C02061	Adult	Vaginal	24469_5_6_bin.27	1485507	84.35	GCA_002893375.1_ASM289337v1	37400776	3.4	0.19	90.53	Cyclospora cayetanensis	Protozoa
21127_6_15	A01011	Adult	Vaginal	21127_6_15_bin.23	2024041	61.74	GCA_002893375.1_ASM289337v1	37400776	3.39	0.15	95.68	Cyclospora cayetanensis	Protozoa
23430_8_24	C02892	Adult	Vaginal	23430_8_24_bin.68	1533772	79.58	GCA_002893375.1_ASM289337v1	37400776	3.3	0.19	90.46	Cyclospora cayetanensis	Protozoa
24469_6_17	B01190	Infancy	Caesarean	24469_6_17_bin.27	1366250	87.87	GCA_002893375.1_ASM289337v1	37400776	3.29	0.14	97.62	Cyclospora cayetanensis	Protozoa
24469_1_22	B01813	Infancy	Vaginal	24469_1_22_bin.18	1538006	78.52	GCA_002893375.1_ASM289337v1	37400776	3.25	0.14	97.4	Cyclospora cayetanensis	Protozoa
14794_3	521130	Neonatal	Vaginal	14794_3_bin.5	1479018	81.83	GCA_002893375.1_ASM289337v1	37400776	3.24	0.13	98.84	Cyclospora cayetanensis	Protozoa
19646_5_9	BBS0038	Adult	Vaginal	19646_5_9_bin.38	1417060	85.14	GCA_002893375.1_ASM289337v1	37400776	3.22	0.17	94.06	Cyclospora cayetanensis	Protozoa
14795_58	606141	Adult	Caesarean	14795_58_bin.23	1557408	77.07	GCA_002893375.1_ASM289337v1	37400776	3.21	0.13	98.69	Cyclospora cayetanensis	Protozoa
25076_4_10	C01512	Infancy	Vaginal	25076_4_10_bin.52	1241044	94.59	GCA_002893375.1_ASM289337v1	37400776	3.21	0.13	97.94	Cyclospora cayetanensis	Protozoa
20596_5_17	B00046	Adult	Vaginal	20596_5_17_bin.28	1421480	83.85	GCA_002893375.1_ASM289337v1	37400776	3.2	0.16	94.22	Cyclospora cayetanensis	Protozoa
23430_8_18	C02868	Adult	Caesarean	23430_8_18_bin.8	1404072	84.46	GCA_002893375.1_ASM289337v1	37400776	3.17	0.17	94.26	Cyclospora cayetanensis	Protozoa
14795_57	514124	Adult	Vaginal	14795_57_bin.16	1359442	87.6	GCA_002893375.1_ASM289337v1	37400776	3.12	0.15	97.05	Cyclospora cayetanensis	Protozoa
21127_6_14	C01052	Adult	Vaginal	21127_6_14_bin.13	1353255	84.01	GCA_002893375.1_ASM289337v1	37400776	3.09	0.20	90.9	Cyclospora cayetanensis	Protozoa
19646_5_3	BBS0014	Neonatal	Vaginal	19646_5_3_bin.14	1542561	74.35	GCA_002893375.1_ASM289337v1	37400776	3.07	0.14	98.59	Cyclospora cayetanensis	Protozoa
22178_6_21	C01962	Adult	Vaginal	22178_6_21_bin.31	1304557	86.93	GCA_002893375.1_ASM289337v1	37400776	3.05	0.14	98.48	Cyclospora cayetanensis	Protozoa
21999_3_15	C01841	Adult	Vaginal	21999_3_15_bin.41	2093157	60.44	GCA_002893375.1_ASM289337v1	37400776	3.02	0.15	95.41	Cyclospora cayetanensis	Protozoa
23430_8_4	C02142	Adult	Caesarean	23430_8_4_bin.6	1906825	60.56	GCA_002893375.1_ASM289337v1	37400776	3.01	0.23	87.5	Cyclospora cayetanensis	Protozoa
21127_4_4	A00539	Adult	Vaginal	21127_4_4_bin.27	1557563	75.52	GCA_002893375.1_ASM289337v1	37400776	2.99	0.18	94.07	Cyclospora cayetanensis	Protozoa
20596_4_6	B00004	Adult	Vaginal	20596_4_6_bin.49	1283383	85.66	GCA_002893375.1_ASM289337v1	37400776	2.99	0.21	90.76	Cyclospora cayetanensis	Protozoa
23430_8_4	C02142	Adult	Caesarean	23430_8_4_bin.43	1358076	83.24	GCA_002893375.1_ASM289337v1	37400776	2.99	0.18	94.03	Cyclospora cayetanensis	Protozoa
23430_8_9	C02391	Adult	Vaginal	23430_8_9_bin.24	1802705	60.99	GCA_002893375.1_ASM289337v1	37400776	2.99	0.21	87.63	Cyclospora cayetanensis	Protozoa
24469_6_19	B01775	Infancy	Vaginal	24469_6_19_bin.52	1307410	82.88	GCA_002893375.1_ASM289337v1	37400776	2.96	0.20	90.95	Cyclospora cayetanensis	Protozoa
25076_5_8	C02345	Infancy	Caesarean	25076_5_8_bin.17	1194219	91.02	GCA_002893375.1_ASM289337v1	37400776	2.96	0.16	94.04	Cyclospora cayetanensis	Protozoa
24469_5_18	B02458	Adult	Caesarean	24469_5_18_bin.2	1291135	84.63	GCA_002893375.1_ASM289337v1	37400776	2.94	0.17	93.99	Cyclospora cayetanensis	Protozoa
21842_4_13	C01560	Adult	Vaginal	21842_4_13_bin.57	1390728	78.18	GCA_002893375.1_ASM289337v1	37400776	2.93	0.22	90.11	Cyclospora cayetanensis	Protozoa
21999_4_20	C01930	Adult	Caesarean	21999_4_20_bin.35	1297955	82.45	GCA_002893375.1_ASM289337v1	37400776	2.91	0.20	90.03	Cyclospora cayetanensis	Protozoa
21999_3_15	C01841	Adult	Vaginal	21999_3_15_bin.21	1386989	77.01	GCA_002893375.1_ASM289337v1	37400776	2.89	0.19	89.53	Cyclospora cayetanensis	Protozoa
23584_5_16	B01948	Adult	Vaginal	23584_5_16_bin.5	1340674	79.75	GCA_002893375.1_ASM289337v1	37400776	2.88	0.19	89.81	Cyclospora cayetanensis	Protozoa
22178_7_1	C01991	Adult	Vaginal	22178_7_1_bin.22	1224978	87.79	GCA_002893375.1_ASM289337v1	37400776	2.85	0.19	93.74	Cyclospora cayetanensis	Protozoa
23584_5_12	B01891	Adult	Vaginal	23584_5_12_bin.29	1341858	78.64	GCA_002893375.1_ASM289337v1	37400776	2.84	0.22	89.53	Cyclospora cayetanensis	Protozoa
25076_6_16	B02752	Infancy	Vaginal	25076_6_16_bin.3	1429969	73.69	GCA_002893375.1_ASM289337v1	37400776	2.82	0.14	98.76	Cyclospora cayetanensis	Protozoa
24469_3_14	B01497	Infancy	Vaginal	24469_3_14_bin.16	1599682	65.34	GCA_002893375.1_ASM289337v1	37400776	2.81	0.15	98.19	Cyclospora cayetanensis	Protozoa
19646_4_4	BBS0070	Neonatal	Caesarean	19646_4_4_bin.15	1207215	85.5	GCA_002893375.1_ASM289337v1	37400776	2.8	0.19	93.04	Cyclospora cayetanensis	Protozoa
24469_4_1	A01015	Adult	Caesarean	24469_4_1_bin.41	1229935	84.82	GCA_002893375.1_ASM289337v1	37400776	2.76	0.17	95.57	Cyclospora cayetanensis	Protozoa
23584_4_24	C02670	Adult	Caesarean	23584_4_24_bin.43	1252024	81.08	GCA_002893375.1_ASM289337v1	37400776	2.76	0.19	90.57	Cyclospora cayetanensis	Protozoa
19646_5_6	BBS0024	Adult	Caesarean	19646_5_6_bin.50	1078149	92.57	GCA_002893375.1_ASM289337v1	37400776	2.73	0.16	96.24	Cyclospora cayetanensis	Protozoa
20727_7_19	B00220	Adult	Vaginal	20727_7_19_bin.6	1143957	87.82	GCA_002893375.1_ASM289337v1	37400776	2.69	0.16	97.71	Cyclospora cayetanensis	Protozoa
20727_7_7	A00163	Adult	Vaginal	20727_7_7_bin.27	1176329	84.03	GCA_002893375.1_ASM289337v1	37400776	2.68	0.15	96.28	Cyclospora cayetanensis	Protozoa
19646_4_11	S10	Adult	Caesarean	19646_4_11_bin.33	1460347	68.29	GCA_002893375.1_ASM289337v1	37400776	2.64	0.19	93.93	Cyclospora cayetanensis	Protozoa
21842_2_9	A01761	Adult	Vaginal	21842_2_9_bin.75	1378980	71.61	GCA_002893375.1_ASM289337v1	37400776	2.62	0.19	90.93	Cyclospora cayetanensis	Protozoa
23584_5_18	B02075	Adult	Vaginal	23584_5_18_bin.33	1216815	80.2	GCA_002893375.1_ASM289337v1	37400776	2.61	0.19	93.66	Cyclospora cayetanensis	Protozoa
23430_8_9	C02391	Adult	Vaginal	23430_8_9_bin.15	1098218	86.75	GCA_002893375.1_ASM289337v1	37400776	2.58	0.22	90.65	Cyclospora cayetanensis	Protozoa
21842_3_8	B01616	Neonatal	Vaginal	21842_3_8_bin.6	2223470	97.48	GCA_900178055.1_L719	2553819	85.65	0.01	99.07	Saccharomyces cerevisiae	Fungi
23430_8_16	C02566	Adult	Caesarean	23430_8_16_bin.18	1061096	87.39	GCA_002893375.1_ASM289337v1	37400776	2.52	0.19	94.53	Cyclospora cayetanensis	Protozoa
21999_3_16	C01844	Neonatal	Vaginal	21999_3_16_bin.18	1175834	78.94	GCA_002893375.1_ASM289337v1	37400776	2.51	0.14	96.73	Cyclospora cayetanensis	Protozoa
14794_3	521130	Neonatal	Vaginal	14794_3_bin.9	1114198	83.36	GCA_002893375.1_ASM289337v1	37400776	2.5	0.17	98.38	Cyclospora cayetanensis	Protozoa
23430_8_8	C02353	Adult	Vaginal	23430_8_8_bin.29	1160416	80.47	GCA_002893375.1_ASM289337v1	37400776	2.5	0.20	90.56	Cyclospora cayetanensis	Protozoa
14794_3	521130	Neonatal	Vaginal	14794_3_bin.13	1229066	74.83	GCA_002893375.1_ASM289337v1	37400776	2.46	0.14	98.42	Cyclospora cayetanensis	Protozoa
21673_42	B00235	Neonatal	Vaginal	21673_42_bin.13	1238513	73.61	GCA_002893375.1_ASM289337v1	37400776	2.43	0.15	98.47	Cyclospora cayetanensis	Protozoa
21127_6_23	C01075	Adult	Vaginal	21127_6_23_bin.35	1125758	80.88	GCA_002893375.1_ASM289337v1	37400776	2.4	0.17	94.67	Cyclospora cayetanensis	Protozoa
14794_4	521130	Neonatal	Vaginal	14794_4_bin.2	1209040	73.3	GCA_002893375.1_ASM289337v1	37400776	2.37	0.14	98.48	Cyclospora cayetanensis	Protozoa
20727_3_18	B00075	Adult	Caesarean	20727_3_18_bin.26	1110519	78.13	GCA_002893375.1_ASM289337v1	37400776	2.37	0.20	90.13	Cyclospora cayetanensis	Protozoa
24469_6_22	B02166	Infancy	Caesarean	24469_6_22_bin.21	1472444	60.07	GCA_002893375.1_ASM289337v1	37400776	2.37	0.18	96.39	Cyclospora cayetanensis	Protozoa
20727_5_9	B00146	Neonatal	Vaginal	20727_5_9_bin.3	1153038	76.13	GCA_002893375.1_ASM289337v1	37400776	2.36	0.14	98.61	Cyclospora cayetanensis	Protozoa
23584_5_13	B01947	Adult	Caesarean	23584_5_13_bin.53	1130261	78.78	GCA_002893375.1_ASM289337v1	37400776	2.36	0.19	95.22	Cyclospora cayetanensis	Protozoa
20596_5_22	B00052	Neonatal	Vaginal	20596_5_22_bin.19	1240504	70.11	GCA_002893375.1_ASM289337v1	37400776	2.33	0.15	98.47	Cyclospora cayetanensis	Protozoa
20727_5_10	B00146	Neonatal	Vaginal	20727_5_10_bin.11	1115109	77.72	GCA_002893375.1_ASM289337v1	37400776	2.33	0.14	98.53	Cyclospora cayetanensis	Protozoa
25076_2_9	B02752	Neonatal	Vaginal	25076_2_9_bin.5	1080484	80.08	GCA_002893375.1_ASM289337v1	37400776	2.33	0.16	97.45	Cyclospora cayetanensis	Protozoa
21999_4_7	C01917	Neonatal	Vaginal	21999_4_7_bin.10	1034869	83.45	GCA_002893375.1_ASM289337v1	37400776	2.32	0.17	96.8	Cyclospora cayetanensis	Protozoa
24469_6_17	B01190	Infancy	Caesarean	24469_6_17_bin.21	937324	88.1	GCA_002893375.1_ASM289337v1	37400776	2.26	0.16	97.69	Cyclospora cayetanensis	Protozoa
20727_4_22	A00105	Neonatal	Caesarean	20727_4_22_bin.5	2245784	95.3	GCA_900178055.1_L719	2553819	84.54	0.01	98.64	Saccharomyces cerevisiae	Fungi
21127_4_14	A00576	Adult	Vaginal	21127_4_14_bin.26	1276049	65.27	GCA_002893375.1_ASM289337v1	37400776	2.24	0.15	97.12	Cyclospora cayetanensis	Protozoa
20596_5_22	B00052	Neonatal	Vaginal	20596_5_22_bin.15	1170457	71.5	GCA_002893375.1_ASM289337v1	37400776	2.23	0.14	98.62	Cyclospora cayetanensis	Protozoa
21673_42	B00235	Neonatal	Vaginal	21673_42_bin.14	1044094	78.57	GCA_002893375.1_ASM289337v1	37400776	2.2	0.17	98.27	Cyclospora cayetanensis	Protozoa
23584_5_18	B02075	Adult	Vaginal	23584_5_18_bin.8	1026360	78.4	GCA_002893375.1_ASM289337v1	37400776	2.18	0.20	89.8	Cyclospora cayetanensis	Protozoa

23430_8_16	C02566	Adult	Caesarean	23430_8_16_bin.16	938815	83.95	GCA_002893375.1_ASM289337v1	37400776	2.17	0.17	95.44	Cyclospora cayetanensis	Protozoa
24211_2_2	C01288	Neonatal	Vaginal	24211_2_2_bin.6	1016027	79.11	GCA_002893375.1_ASM289337v1	37400776	2.16	0.16	97.45	Cyclospora cayetanensis	Protozoa
22178_5_7	B02098	Adult	Caesarean	22178_5_7_bin.60	841277	83.26	GCA_002893375.1_ASM289337v1	37400776	1.9	0.20	93.54	Cyclospora cayetanensis	Protozoa
19646_4_11	S10	Adult	Caesarean	19646_4_11_bin.50	911950	77.13	GCA_002893375.1_ASM289337v1	37400776	1.9	0.26	89.37	Cyclospora cayetanensis	Protozoa
21673_19	A01303	Neonatal	Caesarean	21673_19_bin.12	2184268	92.4	GCA_900178055.1_L719	2553819	79.99	0.01	98.51	Saccharomyces cerevisiae	Fungi
20727_3_18	B00075	Adult	Caesarean	20727_3_18_bin.21	842220	78.72	GCA_002893375.1_ASM289337v1	37400776	1.8	0.21	91.05	Cyclospora cayetanensis	Protozoa
24469_1_18	B01797	Infancy	Vaginal	24469_1_18_bin.28	750086	87.09	GCA_002893375.1_ASM289337v1	37400776	1.8	0.17	95.46	Cyclospora cayetanensis	Protozoa
21242_6	B01190	Neonatal	Caesarean	21242_6_bin.3	2302672	87.75	GCA_900178055.1_L719	2553819	79.86	0.01	98.51	Saccharomyces cerevisiae	Fungi
23430_8_19	A02819	Adult	Caesarean	23430_8_19_bin.9	807985	80.77	GCA_002893375.1_ASM289337v1	37400776	1.77	0.21	90.42	Cyclospora cayetanensis	Protozoa
23584_5_8	C01916	Adult	Vaginal	23584_5_8_bin.21	880662	74.68	GCA_002893375.1_ASM289337v1	37400776	1.74	0.22	93.41	Cyclospora cayetanensis	Protozoa
25076_4_20	C01840	Infancy	Vaginal	25076_4_20_bin.12	723733	80.08	GCA_002893375.1_ASM289337v1	37400776	1.56	0.17	98.37	Cyclospora cayetanensis	Protozoa
22607_3_12	B02315	Neonatal	Caesarean	22607_3_12_bin.2	1713127	93.33	GCA_900178055.1_L719	2553819	63.18	0.01	95.22	Saccharomyces cerevisiae	Fungi
23430_8_17	C02695	Adult	Vaginal	23430_8_17_bin.8	656394	81.32	GCA_002893375.1_ASM289337v1	37400776	1.45	0.20	93.55	Cyclospora cayetanensis	Protozoa
25076_4_10	C01512	Infancy	Vaginal	25076_4_10_bin.13	537505	99.12	GCA_002893375.1_ASM289337v1	37400776	1.43	0.19	97.79	Cyclospora cayetanensis	Protozoa
20727_7_23	A00031	Neonatal	Caesarean	20727_7_23_bin.11	1315462	92.13	GCA_900178055.1_L719	2553819	48.24	0.01	98.03	Saccharomyces cerevisiae	Fungi
20727_5_17	A00106	Adult	Vaginal	20727_5_17_bin.29	815510	64.3	GCA_002893375.1_ASM289337v1	37400776	1.41	0.16	98.21	Cyclospora cayetanensis	Protozoa
22178_5_15	B02118	Neonatal	Vaginal	22178_5_15_bin.1	344401	63.38	GCA_000963415.1_ASM96341v1	15417826	1.39	0.19	99.58	Blastocystis sp.	Protozoa
22607_3_12	B02315	Neonatal	Caesarean	22607_3_12_bin.10	569345	83.71	GCA_900178055.1_L719	2553819	18.82	0.09	96.20	Saccharomyces cerevisiae	Fungi
24469_3_3	B01364	Infancy	Vaginal	24469_3_3_bin.30	301587	67.28	GCA_000963415.1_ASM96341v1	15417826	1.34	0.19	99.47	Blastocystis sp.	Protozoa
24469_6_19	B01775	Infancy	Vaginal	24469_6_19_bin.27	648150	75.18	GCA_002893375.1_ASM289337v1	37400776	1.32	0.24	89.51	Cyclospora cayetanensis	Protozoa
20727_5_10	B00146	Neonatal	Vaginal	20727_5_10_bin.2	640156	74.56	GCA_002893375.1_ASM289337v1	37400776	1.28	0.19	98.41	Cyclospora cayetanensis	Protozoa
23430_8_1	C02186	Adult	Vaginal	23430_8_1_bin.45	521880	88.74	GCA_002893375.1_ASM289337v1	37400776	1.24	0.19	97.96	Cyclospora cayetanensis	Protozoa
14794_8	514123	Neonatal	Vaginal	14794_8_bin.15	541196	82.88	GCA_002893375.1_ASM289337v1	37400776	1.21	0.20	97.93	Cyclospora cayetanensis	Protozoa
21127_6_14	C01052	Adult	Vaginal	21127_6_14_bin.48	598530	72.75	GCA_002893375.1_ASM289337v1	37400776	1.17	0.26	89.27	Cyclospora cayetanensis	Protozoa
23430_8_16	C02566	Adult	Caesarean	23430_8_16_bin.15	655423	60.97	GCA_002893375.1_ASM289337v1	37400776	1.15	0.20	94.66	Cyclospora cayetanensis	Protozoa
20727_7_7	A00163	Adult	Vaginal	20727_7_7_bin.32	223659	74.33	GCA_000963415.1_ASM96341v1	15417826	1.03	0.21	98.46	Blastocystis sp.	Protozoa
23584_5_13	B01947	Adult	Caesarean	23584_5_13_bin.18	205282	75.87	GCA_000963415.1_ASM96341v1	15417826	1.01	0.19	99.27	Blastocystis sp.	Protozoa
24469_6_11	B01710	Infancy	Vaginal	24469_6_11_bin.32	464537	79.03	GCA_002893375.1_ASM289337v1	37400776	1	0.21	90.02	Cyclospora cayetanensis	Protozoa
20727_5_17	A00106	Adult	Vaginal	20727_5_17_bin.8	607293	60.44	GCA_002893375.1_ASM289337v1	37400776	0.99	0.23	98.55	Cyclospora cayetanensis	Protozoa
24469_4_20	A01812	Neonatal	Vaginal	24469_4_20_bin.11	249884	60.79	GCA_000963415.1_ASM96341v1	15417826	0.99	0.19	99.56	Blastocystis sp.	Protozoa
23430_8_24	C02892	Adult	Vaginal	23430_8_24_bin.17	438115	81.2	GCA_002893375.1_ASM289337v1	37400776	0.97	0.26	93.35	Cyclospora cayetanensis	Protozoa
21989_7_19	C01751	Neonatal	Caesarean	21989_7_19_bin.6	212926	68.19	GCA_000963415.1_ASM96341v1	15417826	0.94	0.20	99.91	Blastocystis sp.	Protozoa
21999_3_8	C01840	Neonatal	Vaginal	21999_3_8_bin.14	213224	68.2	GCA_000963415.1_ASM96341v1	15417826	0.94	0.19	99.97	Blastocystis sp.	Protozoa
24469_5_10	C02057	Adult	Caesarean	24469_5_10_bin.38	200474	70.72	GCA_000963415.1_ASM96341v1	15417826	0.94	0.20	99.4	Blastocystis sp.	Protozoa
24469_5_17	C02471	Neonatal	Vaginal	24469_5_17_bin.3	216577	61.79	GCA_000963415.1_ASM96341v1	15417826	0.87	0.20	99.77	Blastocystis sp.	Protozoa
24469_7_3	C02471	Infancy	Vaginal	24469_7_3_bin.1	217523	61.54	GCA_000963415.1_ASM96341v1	15417826	0.87	0.20	99.77	Blastocystis sp.	Protozoa
21673_1	C01329	Adult	Caesarean	21673_1_bin.48	407327	77.5	GCA_002893375.1_ASM289337v1	37400776	0.85	0.26	90.14	Cyclospora cayetanensis	Protozoa
23584_4_24	C02670	Adult	Caesarean	23584_4_24_bin.33	446111	69.42	GCA_002893375.1_ASM289337v1	37400776	0.84	0.23	91.76	Cyclospora cayetanensis	Protozoa
21673_17	B01408	Adult	Vaginal	21673_17_bin.5	208148	62.07	GCA_000963415.1_ASM96341v1	15417826	0.83	0.20	99.58	Blastocystis sp.	Protozoa
21842_2_11	A01763	Adult	Vaginal	21842_2_11_bin.10	325892	89.09	GCA_002893375.1_ASM289337v1	37400776	0.79	0.23	92.82	Cyclospora cayetanensis	Protozoa
21999_3_9	C01840	Neonatal	Vaginal	21999_3_9_bin.13	303384	88.02	GCA_002893375.1_ASM289337v1	37400776	0.72	0.21	96.8	Cyclospora cayetanensis	Protozoa
21842_3_23	B01719	Adult	Vaginal	21842_3_23_bin.4	270791	90.88	GCA_002893375.1_ASM289337v1	37400776	0.69	0.24	95.48	Cyclospora cayetanensis	Protozoa
14795_55	519129	Adult	Caesarean	14795_55_bin.75	487540	60.43	GCA_002893375.1_ASM289337v1	37400776	0.65	0.21	97.66	Cyclospora cayetanensis	Protozoa
21127_3_2	B00238	Adult	Caesarean	21127_3_2_bin.10	338659	71.18	GCA_002893375.1_ASM289337v1	37400776	0.65	0.24	98.67	Cyclospora cayetanensis	Protozoa
22178_3_17	A02064	Adult	Caesarean	22178_3_17_bin.12	204226	65.99	GCA_000963415.1_ASM96341v1	15417826	0.63	0.24	94.01	Blastocystis sp.	Protozoa
14795_56	513122	Adult	Vaginal	14795_56_bin.19	318870	65.45	GCA_002893375.1_ASM289337v1	37400776	0.58	0.22	91.46	Cyclospora cayetanensis	Protozoa
24469_5_22	A01506	Infancy	Caesarean	24469_5_22_bin.22	299371	64.16	GCA_002893375.1_ASM289337v1	37400776	0.56	0.22	96.92	Cyclospora cayetanensis	Protozoa
24469_6_17	B01190	Infancy	Caesarean	24469_6_17_bin.28	286344	64.1	GCA_002893375.1_ASM289337v1	37400776	0.55	0.26	95.3	Cyclospora cayetanensis	Protozoa
22607_3_12	B02315	Neonatal	Caesarean	22607_3_12_bin.5	376454	97.58	GCA_900178055.1_L719	2553819	7.6	0.13	94.43	Saccharomyces cerevisiae	Fungi
24469_3_21	B02284	Infancy	Caesarean	24469_3_21_bin.4	208707	96.07	GCA_002893375.1_ASM289337v1	37400776	0.54	0.24	97.95	Cyclospora cayetanensis	Protozoa
21673_20	C01443	Adult	Caesarean	21673_20_bin.44	289956	69.45	GCA_002893375.1_ASM289337v1	37400776	0.54	0.24	98.38	Cyclospora cayetanensis	Protozoa
19646_4_12	S13	Adult	Vaginal	19646_4_12_bin.47	207708	87.89	GCA_002893375.1_ASM289337v1	37400776	0.5	0.24	95.52	Cyclospora cayetanensis	Protozoa
14794_3	521130	Neonatal	Vaginal	14794_3_bin.1	260298	66.68	GCA_002893375.1_ASM289337v1	37400776	0.46	0.26	98.76	Cyclospora cayetanensis	Protozoa
20727_5_17	A00106	Adult	Vaginal	20727_5_17_bin.2	282038	60.18	GCA_002893375.1_ASM289337v1	37400776	0.46	0.23	98.67	Cyclospora cayetanensis	Protozoa
25076_3_24	B02320_T1	Infancy	Vaginal	25076_3_24_bin.1	265639	61.1	GCA_002893375.1_ASM289337v1	37400776	0.45	0.22	99.67	Cyclospora cayetanensis	Protozoa
24469_4_1	A01015	Adult	Caesarean	24469_4_1_bin.60	212924	61.42	GCA_002893375.1_ASM289337v1	37400776	0.36	0.23	96	Cyclospora cayetanensis	Protozoa
22178_7_16	C02047	Adult	Caesarean	22178_7_16_bin.4	206128	63.23	GCA_002893375.1_ASM289337v1	37400776	0.36	0.26	88.64	Cyclospora cayetanensis	Protozoa